

## SEQUENCE LISTING

*INS  
B*

<110> AUJAME et al.

<120> Nucleic acids and polypeptides specific for pathogenic strains of the Neisseria genus

<130> P07180US00/BAS

<140> 09/830, 433

<141> 2001-04-26

<150> FR 98 13 693

<151> 1998-10-30

<160> 129

<170> PatentIn Ver. 2.1

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<213> Neisseria meningitidis

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cat ttg ggt gta aag atg tat tcg cac lac gtt cct gcg att gcc gag	96
His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu	
20                   25                   30	

ttg ata gcg aat gcc tac gat gca tgc ttt gct aag gaa gtg gaa gtt agg	144
Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg	
35                   40                   45	

tta ttc gat aaa ccg gag cat aaa atc gtt atc aat gat aat ggt ata	192
Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile	
50                   55                   60	

gga atg agc ttc gat gaa atc aat gat ttt tat ttg aag aac ggt cgg	240
Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg	
65                   70                   75                   80	

aac aga agg gaa gaa aaa caa gct tcc ccg tgc gga aga aac cca acg	288
Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr	
85                   90                   95	

ggt aaa aaa ggc ctt ggt aaa ttg gca tta ttc ggg ctt ggc aac aaa	336
Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Gly Leu Gly Asn Lys	
100                   105                   110	

att gaa att tct act atc cag gga aac gaa agg gtt act ttt act ttg	384
Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu	
115                   120                   125	

gat tat gca gag att cga aga agc aag ggt att tat caa ccg gag ttt	432
Asp Tyr Ala Glu Ile Arg Arg Ser Lys Gly Ile Tyr Gln Pro Glu Phe	
130                   135                   140	

cga aaa gaa tct gtt gaa tcc aat atc gaa agc ggg aca acc ata act 480  
Arg Lys Glu Sér Val' Ser Asn Ile Glu Ser Gly Thr Thre Thr  
145 155 160

tta acc gaa ctg acg aaa aag caa gga tat ccg tta gat aat tat gta 528  
Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val  
165 170 175

gag cat ctt tcc cgc ttg ttt gat ttt ccg gct cag gat ttt aaa atc 576  
Glu His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile  
180 185 190

aaa gta agc ttg aac ggc tct gaa cct aaa atc att gat gga aat cta 624  
Lys Val Ser Leu Asn Gly Ser Glu Pro Lys Ile Ile Asp Gly Asn Leu  
195 200 205

aaa tat gat ctt gtt acc cca caa ttc gaa tgg gaa tac cag gat tta 672  
Lys Tyr Asp Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu  
210 215 220

gca acc aat att tca tcg tta tct tca aaa ttc gaa cag tat gaa tac 720  
Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr  
225 230 235 240

agc gga tta ata caa ggt aag ttc att aca acg gaa aaa cct tta aag 768  
Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys  
245 250 255

aat aat atg aaa ggt att acc ttg ttt gcc aac ggc aga atg gta aat 816  
Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn  
260 265 270

atg ccc gag ttt ttc act gat agc gaa tcc agc cat ttc taa 858  
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35 40 45

Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile  
50 55 60

Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg  
65 70 75 80

Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr  
85 90 95

Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Gly Leu Gly Asn Lys  
100 105 110

Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu  
115 120 125

Asp Tyr Ala Glu Ile Arg Ser Lys Gly Ile Tyr Gln Pro Phe  
130 135 140

Arg Lys Glu Ser Val Glu Ser Asn Ile Glu Ser Gly Thr Thr Ile Thr  
145 150 155 160

Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val  
165 170 175

Glu His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile  
180 185 190

Lys Val Ser Leu Asn Gly Ser Glu Pro Lys Ile Ile Asp Gly Asn Leu  
195 200 205

Lys Tyr Asp Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu  
210 215 220

Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr  
225 230 235 240

Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys  
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gac aaa tta cta acc gaa aat acc cat att tgg cta ttt ata ggt gta 96  
Asp Lys Leu Leu Thr Glu Asn Thr His Ile Trp Leu Phe Ile Gly Val  
20 25 30

tta cac aaa atg tta cct att agt ctg gtg caa tcc cta cta cgt ttc 144  
Leu His Lys Met Leu Pro Ile Ser Leu Val Gln Ser Leu Leu Arg Phe  
35 40 45

ggc gaa cgt gtc cat ctt gtc cag tta caa aaa acg ggg aaa aac gca 192  
Gly Glu Arg Val His Leu Val Gln Leu Gln Lys Thr Gly Lys Asn Ala  
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ttg gat ttt tac ctg tcc tat tac ctc gga caa att acc gcc aca gac 240  
Leu Asp Phe Tyr Leu Ser Tyr Tyr Leu Gly Gln Ile Thr Ala Thr Asp  
65 70 75 80

ccc aat gcc caa atc ggc ata ctc tcg cgt gat gga gga tac gat gtt 288  
Pro Asn Ala Gln Ile Gly Ile Leu Ser Arg Asp Gly Gly Tyr Asp Val  
85 90 95

ctg gtc gaa cat att [REDACTED] aaa aac cac cag gcg aag ggt at [REDACTED] g cgc	336
Leu Val Glu His Ile [REDACTED] Lys Asn His Gln Ala Lys Gly Ile [REDACTED] Arg	
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cta gcc aat ata gat gaa gta caa cat cag aaa att gct acc gaa ccg	384
Leu Ala Asn Ile Asp Glu Val Gln His Gln Lys Ile Ala Thr Glu Pro	
115 120 125	
ccg tca gca ttg ctg gaa aac act cct cag cct gaa acc acc ctc aaa	432
Pro Ser Ala Leu Leu Glu Asn Thr Pro Gln Pro Glu Thr Thr Leu Lys	
130 135 140	
cca cag caa cca tta act tcc tat ttc caa gca gcc cta act gca ctg	480
Pro Gln Gln Pro Leu Thr Ser Tyr Phe Gln Ala Ala Leu Thr Ala Leu	
145 150 155 160	
cgc cgc ccc gac gct ttc cgc ccc tgc cgc ctg cat aac ctg cga caa	528
Arg Arg Pro Asp Ala Phe Arg Pro Cys Arg Leu His Asn Leu Arg Gln	
165 170 175	
aat ctg cgt aag cat att ttg agt gat ttg ttt aaa gaa aaa acc gat	576
Asn Leu Arg Lys His Ile Leu Ser Asp Leu Phe Lys Glu Lys Thr Asp	
180 185 190	
gaa gaa tgc gaa ata acc act gct aac gtt atc aat aaa ctc aaa gca	624
Glu Glu Cys Glu Ile Thr Thr Ala Asn Val Ile Asn Lys Leu Lys Ala	
195 200 205	
caa aac ttc atc agc att gat gaa cag gaa acc gtt tcc tac cat ctc	672
Gln Asn Phe Ile Ser Ile Asp Glu Gln Glu Thr Val Ser Tyr His Leu	
210 215 220	
agt gat aat gat ttg tta caa aga atc caa cgc cat att tta agc caa	720
Ser Asp Asn Asp Leu Leu Gln Arg Ile Gln Arg His Ile Leu Ser Gln	
225 230 235 240	
cgt ccc aaa acc tac gct gat ttt caa gcc gtc gtg caa aac cga gca	768
Arg Pro Lys Thr Tyr Ala Asp Phe Gln Ala Val Val Gln Asn Arg Ala	
245 250 255	
gat gca ctt cac tta aca gtc ggt acc aac gac att caa tcc ttt gcg	816
Asp Ala Leu His Leu Thr Val Gly Thr Asn Asp Ile Gln Ser Phe Ala	
260 265 270	
cga cat ttg cgc gac caa aac ctg atc cgc caa aac aat ggg aaa att	864
Arg His Leu Arg Asp Gln Asn Leu Ile Arg Gln Asn Asn Gly Lys Ile	
275 280 285	
gaa tat gca ccg ttt act gaa cct aaa cca cag cca acg ccc aag cag	912
Glu Tyr Ala Pro Phe Thr Glu Pro Lys Pro Gln Pro Thr Pro Lys Gln	
290 295 300	
cct aaa aaa acc gca tgg gaa cct gat gaa att att tgg aaa aaa gtg	960
Pro Lys Lys Thr Ala Trp Glu Pro Asp Glu Ile Ile Trp Lys Lys Val	
305 310 315 320	
att gcc gcg tta tcg tta aag aac cgt cct aat aaa acc aaa act tta	1008
Ile Ala Ala Leu Ser Leu Lys Asn Arg Pro Asn Lys Thr Lys Thr Leu	
325 330 335	
cgc aat aca atc cag gca ctc aca aaa tcc aat gca caa gaa act gac	1056
Arg Asn Thr Ile Gln Ala Leu Thr Lys Ser Asn Ala Gln Glu Thr Asp	
340 345 350	
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Leu His Lys Met Leu Pro Ile Ser Leu Val Gln Ser Leu Leu Arg Phe  
35 40 45

Gly Glu Arg Val His Leu Val Gln Leu Gln Lys Thr Gly Lys Asn Ala  
50 55 60

Leu Asp Phe Tyr Leu Ser Tyr Tyr Leu Gly Gln Ile Thr Ala Thr Asp  
65 70 75 80

Pro Asn Ala Gln Ile Gly Ile Leu Ser Arg Asp Gly Gly Tyr Asp Val  
85 90 95

Leu Val Glu His Ile Leu Lys Asn His Gln Ala Lys Gly Ile Val Arg  
100 105 110

Leu Ala Asn Ile Asp Glu Val Gln His Gln Lys Ile Ala Thr Glu Pro  
115 120 125

Pro Ser Ala Leu Leu Glu Asn Thr Pro Gln Pro Glu Thr Thr Leu Lys  
130 135 140

Pro Gln Gln Pro Leu Thr Ser Tyr Phe Gln Ala Ala Leu Thr Ala Leu  
145 150 155 160

Arg Arg Pro Asp Ala Phe Arg Pro Cys Arg Leu His Asn Leu Arg Gln  
165 170 175

Asn Leu Arg Lys His Ile Leu Ser Asp Leu Phe Lys Glu Lys Thr Asp  
180 185 190

Glu Glu Cys Glu Ile Thr Thr Ala Asn Val Ile Asn Lys Leu Lys Ala  
195 200 205

Gln Asn Phe Ile Ser Ile Asp Glu Gln Glu Thr Val Ser Tyr His Leu  
210 215 220

Ser Asp Asn Asp Leu Leu Gln Arg Ile Gln Arg His Ile Leu Ser Gln  
225 230 235 240

Arg Pro Lys Thr Tyr Ala Asp Phe Gln Ala Val Val Gln Asn Arg Ala  
245 250 255

Asp Ala Leu His Leu Thr Val Gly Thr Asn Asp Ile Gln Ser Phe Ala  
260 265 270

Arg His Leu Arg Asp Gln Asn Leu Ile Arg Gln Asn Asn Gly Lys Ile  
275 280 285

Glu Tyr Ala Pro Phe Thr Glu Pro Lys Pro Gln Pro Thr Pro Lys Gln  
290 295 300

Pro Lys Lys Thr Ala Glu Pro Asp Glu Ile Ile Trp Lys Lys Val  
305 315 320

Ile Ala Ala Leu Ser Leu Lys Asn Arg Pro Asn Lys Thr Lys Thr Leu  
325 330 335

Arg Asn Thr Ile Gln Ala Leu Thr Lys Ser Asn Ala Gln Glu Thr Asp  
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Lys Leu Leu Gln His Leu Gln Asp Asp Pro Ser Pro Thr Tyr  
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gcc agc gaa atc gcc tat cgc ttt gta ttc gga att gaa acc tta ccg 96  
Ala Ser Glu Ile Ala Tyr Arg Phe Val Phe Gly Ile Glu Thr Leu Pro  
20 25 30

gct gca aaa atg gca gaa acg ttt gcg ctg aca ttt atg att gct gcg 144  
- Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala  
35 40 45

- ctg tat ctg ttt gcg cgt tat aag gct tcg cgg ctg ctg att gcg gtg 192  
Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val  
50 55 60

ttt ttc gcg ttc acg att att gcc aac aat gta cat tat gcg gtt tat 240  
Phe Phe Ala Phe Ser Ile Ile Ala Asn Asn Val His Tyr Ala Val Tyr  
65 70 75 80

caa agt tgg atg acg ggc atc aat tat tgg ctg atg ctg aaa gag att 288  
Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Ile  
85 90 95

acc gaa gtc ggc agt gcg ggc tcg atg ttg gat aag ttg tgg ctg 336  
Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu  
100 105 110

cct gcg ttg tgg ggc gtg ttg gaa gtc atg ttg ttt tgc agc ctt gcc 384  
Pro Ala Leu Trp Gly Val Leu Glu Val Met Leu Phe Cys Ser Leu Ala  
115 120 125

aag ttc cac cgt aag acg cat ttt tct gcc gat ata ctg ttt gcc ttc 432  
Lys Phe His Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe  
130 135 140

cta atg ctg atg att ttc gtg cgt tcg ttc gac acg aaa caa gag cac 480  
Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His  
145 150 155 160

ggt att tcg ccc aaa ccg aca tac agc cgc atc aaa gcc aat tat ttc 528

Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe			
165	170	175	
agc ttc ggt tat ttt gtc gga cgc gtg ttg ccg tat cag ttg ttt gat			576
Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp			
180	185	190	
tta agc agg att ccc gcc ttt aag cag cct gct cca agc aaa atc ggg			624
Leu Ser Arg Ile Pro Ala Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly			
195	200	205	
cag ggc agt gtt caa aat atc gtc ctg att atg ggc gaa agc gaa agc			672
Gln Gly Ser Val Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser			
210	215	220	
gcg gcg cat ttg aag ctg ttt ggc tac gga cgc gaa act tcg ccg ttt			720
Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe			
225	230	235	240
tta acc cgg ctg tcg caa gcc gat ttt aag ccg att gtg aaa caa agt			768
Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser			
245	250	255	
tat tcc gca ggc ttt atg act gca gtg tcc ctg ccc agt ttt ttc aat			816
Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn			
260	265	270	
gcg ata ccg cac gcc aac ggc ttg gaa caa atc agc ggc ggc gat act			864
Ala Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr			
275	280	285	
aat atg ttc cgc ctc gcc aaa gag cag ggc tat gaa acg tat ttt tac			912
Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr			
290	295	300	
agc gca cag gcg gaa aac gag atg gcg att ttg aac tta atc ggt aag			960
Ser Ala Gln Ala Glu Asn Glu Met Ala Ile Leu Asn Leu Ile Gly Lys			
305	310	315	320
aaa tgg ata gac cat ctg att cag ccg acg cag ctt ggc tac ggc aac			1008
Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn			
325	330	335	
ggc gac aat atg ccc gat gag aag ctg ctg ccg ctg ttc gac aaa atc			1056
Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile			
340	345	350	
aat ttg cag cag ggc agg cat ttt atc gtg ttg cac caa cgt ggt tcg			1104
Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser			
355	360	365	
cac gcc cca tac agc gca ttg ttg cag cct caa gat aaa gta ttc ggc			1152
His Ala Pro Tyr Ser Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly			
370	375	380	
gaa ctt att gtg gat aag tac gac aac acc atc cac aaa acc gac caa			1200
Glu Leu Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp Gln			
385	390	395	400
atg att caa acc gta ttc gag cag ctg caa aag cag cct gac ggc aac			1248
Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly Asn			
405	410	415	
tgg ctg ttt gcc tat acc tcc gat cat ggc cag tat gtt cgc caa gat			1296
Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln Asp			
420	425	430	

atc tac aat caa ggc	gtg cag ccc gac agc tat ctc gt	ctg	1344
Ile Tyr Asn Gln Gly	Val Gln Pro Asp Ser Tyr Leu Val	Leu	
435	440	445	
gtg ttg tac agc tcg aat aag gcc	gtg caa cag gct gcc aac cag gct		1392
Val Leu Tyr Ser Ser Asn Lys	Ala Val Gln Gln Ala Ala Asn Gln Ala		
450	455	460	
ttt gcg cct tgc gag att gcc ttc cat cag cag ctt tca acg ttc ctg			1440
Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe Leu			
465	470	475	480
att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa ggc			1488
Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu Gly			
485	490	495	
tcg gta acg ggc aac ctg att acg ggt gat gca ggc agc ttg aac att			1536
Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn Ile			
500	505	510	
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Arg Asp Gly Lys Ala Glu Tyr Val Tyr Pro Gln			
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Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala			
35	40	45	

Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val			
50	55	60	

Phe Phe Ala Phe Ser Ile Ile Ala Asn Asn Val His Tyr Ala Val Tyr			
65	70	75	80

Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Ile			
85	90	95	

Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu			
100	105	110	

Pro Ala Leu Trp Gly Val Leu Glu Val Met Leu Phe Cys Ser Leu Ala			
115	120	125	

Lys Phe His Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe			
130	135	140	

Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His			
145	150	155	160

Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe			
165	170	175	

Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp

DRAFTED BY: S. S. KUMAR

180                    185                    190

Leu Ser Arg Ile Pro Phe Lys Gln Pro Ala Pro Ser Ly Le Gly  
195                    200                    205

Gln Gly Ser Val Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser  
210                    215                    220

Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe  
225                    230                    240

Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser  
245                    250                    255

Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn  
260                    265                    270

Ala Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr  
275                    280                    285

Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr  
290                    295                    300

Ser Ala Gln Ala Glu Asn Glu Met Ala Ile Leu Asn Leu Ile Gly Lys  
305                    310                    320

Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn  
325                    330                    335

Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile  
340                    345                    350

Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser  
355                    360                    365

His Ala Pro Tyr Ser Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly  
370                    375                    380

Glu Leu Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp Gln  
385                    390                    400

Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly Asn  
405                    410                    415

Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln Asp  
420                    425                    430

Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Leu Val Pro Leu  
435                    440                    445

Val Leu Tyr Ser Ser Asn Lys Ala Val Gln Gln Ala Ala Asn Gln Ala  
450                    455                    460

Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe Leu  
465                    470                    480

Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu Gly  
485                    490                    495

Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn Ile  
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Arg Asp Gly Lys Ala Glu Tyr Val Tyr Pro Gln  
515                    520

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 Met Ala Leu Ala Val Ala Thr Thr Leu Ser Ala Cys Leu Gly Gly Gly  
 20 25 30

ggc ggc act tct gcg ccc gac ttc aat gca ggc ggc acc ggt atc ggc  
 Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly  
 35 40 45

agc aac agc aga gca aca aca gcg aaa tca gca gca gta tct tac gcc  
 Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala  
 50 55 60

ggt atc aag aac gaa atg tgc aaa gac aga agc atg ctc tgt gcc ggt  
 Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly  
 65 70 75 80

cgg gat gac gtt gcg gtt aca gac agg gat gcc aaa atc aat gcc ccc  
 Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro  
 85 90 95

ccc ccg aat ctg cat acc gga gac ttt aca aac cca aat gac gca tac  
 Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn Pro Asn Asp Ala Tyr  
 100 105 110

aag aat ttg atc aac ctc aaa cct gca att gaa gca ggc tat aca gga  
 Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly  
 115 120 125

cgc ggg gta gag gta ggt atc gtc gat aca ggc gaa tcc gtc ggc agc  
 Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser  
 130 135 140

ata tcc ttt ccc gaa ctg tat ggc aga aaa gaa cac ggc tat aac gaa  
 Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu  
 145 150 155 160

aat tac aaa aac tat acg gcg tat atg cgg aag gaa gcg cct gaa gac  
 Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp  
 165 170 175

gga ggc ggt aaa gac att aaa gct tct ttc gac gat gag gcc gtt ata  
 Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile  
 180 185 190

gag act gaa gca aag ccg acg gat atc cgc cac gta aaa gaa atc gga  
 Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly  
 195 200 205

cac atc gat gtg gtc tcc cat att att ggc ggg cgt tcc gtg gac ggc  
 His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly  
 210 215 220

aga cct gca ggc ggt.	gag	ccc gat gcg acg cta cac atg aat	720
Arg Pro Ala Gly Gly		Ala Pro Asp Ala Thr Leu His Ile Met Asn	
225	230	235	240
acg cat gat gga acc aag aac gaa ata atg tct gca gcc atc cgc aat			768
Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser Ala Ala Ile Arg Asn			
245	250	255	
gca tgg gtc aag ctg ggc gaa cgt ggc gtg cgc atc gtc aat aac agt			816
Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser			
260	265	270	
ttt gga aca aca tcg agg gca ggc act gcc gac cat ttc caa ata gcc			864
Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp His Phe Gln Ile Ala			
275	280	285	
aat tcg gag gag cag tac cgc caa gcg ttg ctc gcc tat tcc ggc ggt			912
Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Ala Tyr Ser Gly Gly			
290	295	300	
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Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly			
305	310	315	320
aac ttg tcc tac cac atc cgt aat aaa aac atg ctt ttc att ttt tcg			1008
Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser			
325	330	335	
gca agc aat gac gca caa gct cag ccc aac aca ctg acc cta ttg cca			1056
Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr Leu Thr Leu Leu Pro			
340	345	350	
ttt tat gaa aaa gat gct caa aaa ggc att atc aca gtc gca ggc gta			1104
Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val			
355	360	365	
gac cgc agt gga gaa aag ttc aat ggc tcc aac cat tgc gga att act			1152
Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn His Cys Gly Ile Thr			
370	375	380	
gcc atg tgg tgc cta tcg gca ccc tat gaa gca agc gtc cgt ttc acc			1200
Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr			
385	390	395	400
cgt aca aac ccg att caa att gcc gga aca tcc ttt tcc gca ccc atc			1248
Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile			
405	410	415	
gta acc ggc acg gcg gct ctg ctg ctg cag aaa tac ccg tgg atg agc			1296
Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser			
420	425	430	
aac gac aac ctg cgt acc acg ctg ctg aca acg gct cag gac atc ggt			1344
Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly			
435	440	445	
gca gtc ggc gtg gac agc aag ttc ggc tgg gga ctg ctg gat gcg ggt			1392
Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly			
450	455	460	
aag gcc atg aac gga ccc gcg tcc ttt ccg ttc ggc gac ttt acc gcc			1440
Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala			
465	470	475	480
gat acg aaa ggt aca tcc gat att gcc tac tcc ttc cgt aac gac att			1488

Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile  
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tca ggc acg ggc ggc ctg atc aaa aaa ggc ggc agc caa ctg caa ctg	1536
Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Ser Gln Leu Gln Leu	
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cac ggc aac aac acc tat acg ggc aaa acc att atc gaa ggc ggt tcg	1584
His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Ser	
515 520 525	
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Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys	
530 535 540	
ggt gcg ctg att tat aac ggg gcg gca tcc ggc ggt agc ctg aac agc	1680
Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser	
545 550 555 560	
gac ggc att gtc tat ctg gca gat acc gac cga tcc ggc gca aac gaa	1728
Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg Ser Gly Ala Asn Glu	
565 570 575	
acc gtg cac atc aaa ggc gat ctg cag ctg ggc ggc gaa ggt acg ctg	1776
Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly Glu Gly Thr Leu	
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Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Met Thr	
595 600 605	
ggc ggc aag ctg tac atg tcg gca cgc ggc aaa ggg gca ggc tat ctc	1872
Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu	
610 615 620	
aac cgt acc gga caa cgt gtt ccc ttc ctg agt gcc gcc aaa atc ggg	1920
Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly	
625 630 635 640	
cgg gat tat tct ttc aca aac atc gaa acc gac ggt ggt ctg ctg	1968
Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu	
645 650 655	
gct tcc ctc gac agc gtc gaa aaa aca gcg ggc agt gaa ggc gac acg	2016
Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr	
660 665 670	
ctg tcc tat tat gtc cgt cgc ggc aat gcg gca cggt act gct tcg gca	2064
Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala	
675 680 685	
gcg gca cat tcc gcg ccc gcc ggt ctg aaa cac gcc gta gaa cag ggc	2112
Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly	
690 695 700	
ggc agc aat ctg gaa aac ctg atg gtc gaa ctg gat gcc tcc gaa tca	2160
Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser	
705 710 715 720	
tcc gca aca ccc gag acg gtt gaa act gcg gcc gcc gac cgc aca gat	2208
Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp	
725 730 735	
atg ccg ggc atc cgc ccc tac ggc gca act ttc cgc gca gcg gca gcc	2256
Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala	
740 745 750	

gta cag cat gcg aat.	██████████	gcc gac ggt gta cgc atc ttc aa	██████████	gt ctc	2304
Val Gln His Ala Asn	██████████	Ala Asp Gly Val Arg Ile Phe Asp	██████████	Leu	
755	760	765			
gcc gct acc gtc tat gcc gac agt acc gcc cat gcc gat atg cag					2352
Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln					
770	775	780			
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Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr					
785	790	795	800		
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Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu					
805	810	815			
cag ggc ggt gtt gaa ggc aaa atg cgc ggc agt acc caa acc gtc ggc					2496
Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly					
820	825	830			
att gcc gcg aaa acc ggc gaa aat acg aca gca gcc gcc aca ctg ggc					2544
Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly					
835	840	845			
atg gga cac agc aca tgg agc gaa aac agt gca aat gca aaa acc gac					2592
Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp					
850	855	860			
agc att agt ctg ttt gca ggc ata cgg cac gat gcg ggc gat atc ggc					2640
Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly					
865	870	875	880		
tat ctc aaa ggc ctg ttc tcc tac gga cgc tac aaa aac agc atc agc					2688
Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser					
885	890	895			
cg <sup>c</sup> agc acc ggt gcg gac gaa cat gcg gaa ggc agc gtc aac ggc acg					2736
Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr					
900	905	910			
ctg atg cag ctg ggc gca ctg ggc ggt gtc aac gtt ccg ttt gcc gca					2784
Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala					
915	920	925			
acg gga gat ttg acg gtc gaa ggc ggt ctg cgc tac gac ctg ctc aaa					2832
Thr Gly Asp Leu Thr Val Glu Gly Leu Arg Tyr Asp Leu Leu Lys					
930	935	940			
cag gat gca ttc gcc gaa aaa ggc agt gct ttg ggc tgg agc ggc aac					2880
Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn					
945	950	955	960		
agc ctc act gaa ggc aca ctg gga ctc gcg ggt ctg aag ctg tcg					2928
Ser Leu Thr Glu Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser					
965	970	975			
caa ccc ttg agc gat aaa gcc gtc ctg ttt gca acg gcg ggc gtg gaa					2976
Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu					
980	985	990			
cgc gac ctg aac gga cgc gac tac acg gta acg ggc ggc ttt acc ggc					3024
Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly					
995	1000	1005			
g <sup>c</sup> g act gca gca acc ggc aag acg ggg gca cgc aat atg ccg cac acc					3072

Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr  
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 Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp  
 1025 1030 1035 1040  
 aac ggc ttg gca cgt tac agc tac gcc ggt tcc aaa cag tac ggc aac 3168  
 Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn  
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 Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly  
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 Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala  
 50 55 60  
  
 Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly  
 65 70 75 80  
  
 Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro  
 85 90 95  
  
 Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn Pro Asn Asp Ala Tyr  
 100 105 110  
  
 Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly  
 115 120 125  
  
 Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser  
 130 135 140  
  
 Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu  
 145 150 155 160  
  
 Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp  
 165 170 175  
  
 Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile  
 180 185 190  
  
 Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly  
 195 200 205  
  
 His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly  
 210 215 220  
  
 Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn  
 225 230 235 240

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Thr His Asp Gly Thr. 245 Asn Glu Ile Met Ser Ala Ala Ile Arg Asn  
250 255

Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser  
260 265 270

Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp His Phe Gln Ile Ala  
275 280 285

Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Ala Tyr Ser Gly Gly  
290 295 300

Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly  
305 310 315 320

Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser  
325 330 335

Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr Leu Thr Leu Leu Pro  
340 345 350

Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val  
355 360 365

Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn His Cys Gly Ile Thr  
370 375 380

Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr  
385 390 395 400

Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile  
405 410 415

Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser  
420 425 430

Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly  
435 440 445

Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly  
450 455 460

Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala  
465 470 475 480

Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile  
485 490 495

Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu  
500 505 510

His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser  
515 520 525

Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys  
530 535 540

Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser  
545 550 555 560

Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg Ser Gly Ala Asn Glu  
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Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly Gly Glu Gly Thr Leu  
580 585 590

DRAFT

Tyr Thr Arg Leu Gly. [ ] Leu Leu Lys Val Asp Gly Thr Ala [ ] Met Thr  
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Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu  
610 615 620

Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly  
625 630 635 640

Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu  
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Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr  
660 665 670

Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala  
675 680 685

Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly  
690 695 700

Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser  
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Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala  
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Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu  
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Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln  
770 775 780

Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr  
785 790 795 800

Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu  
805 810 815

Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly  
820 825 830

Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly  
835 840 845

Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp  
850 855 860

Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly  
865 870 875 880

Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser  
885 890 895

Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr  
900 905 910

Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala  
915 920 925

Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys  
930 935 940

Gln Asp Ala Phe Ala Lys Gly Ser Ala Leu Gly Trp Ser Asn  
 945 955 960

Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser  
 965 970 975

Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu  
 980 985 990

Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly  
 995 1000 1005

Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr  
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Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp  
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His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe  
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gca ggt tgc ggc tca atc aat aat gta acc gtt tcc gac cag aaa ctt	96
Ala Gly Cys Gly Ser Ile Asn Asn Val Thr Val Ser Asp Gln Lys Leu	
20 25 30	

cag gaa cgt gcc gcg ttt gcc ttg ggc gtc agc caa aat gcc gta aaa	144
Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys	
35 40 45	

atc agc aac cgc agc aat gaa agc ata cgc atc aac ttt acc gca act	192
Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr	
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gtg ggt aag cgc gtg agc caa tgc tat gtt acc agt gta atc agc aca	240
Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr	
65 70 75 80	

atc ggc gtt acc act tcc gat gca att tgt ttg gga ggc gga acg cac	288
Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Thr His	
85 90 95	

aaa ggc aaa agt caa tgc aat gct ttg ctt aaa gcg gca ggc cgt tgc	336
Lys Gly Lys Ser Gln Cys Asn Ala Leu Leu Lys Ala Ala Gly Arg Cys	
100 105 110	

taa

339

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Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys  
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Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr  
50 55 60  
  
Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr  
65 70 75 80  
  
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1 5 10 15  
  
ctg ctg acg gaa aaa gtg tcg ccc atc atc gca tta atc ttg gtg ccg 96  
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Leu Phe Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu  
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Phe Tyr Ser Gly Gly Thr Lys Ser Val Met Gln Ile Val Ile Met Phe  
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atg ttt tcc att ttg ttt ttt gga atc atg aac gat gtg ggg ctg ttc 240  
Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe  
65 70 75 80  
  
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Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val  
85 90 95  
  
gca gtg agt gtg ggg acg gtc ttg gtg tcg gtg gtg gcg cag ttg gac 336

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Gly Ala Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro			
115	120	125	
ctt tac aag cgt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg			432
Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu			
130	135	140	
act tcc agt gcg gga ttg att aac ctt ctg ccg tgg ggc ggg ccg acc			480
Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Trp Gly Gly Pro Thr			
145	150	155	160
ggg cgg gtt gca agc gtg ttg ggc gca gat gtg ggc gaa ttg tat aaa			528
Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys			
165	170	175	
cct ttg ttg acg gtg caa att atc ggt gtg gtg ttt atc ctt gcg ctg			576
Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Ala Leu			
180	185	190	
tcc ctg ctt ttg ggt gtg cgt gaa aaa agg ccg att gtc ccg gag ttg			624
Ser Leu Leu Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu			
195	200	205	
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Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Val Pro Leu Ser			
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Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val			
225	230	235	240
ctg ctg ttt ttg gcg gcg atg agc ctg ctt ttt tcg ggc atc ttc ccg			768
Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro			
245	250	255	
ccg ggt tat gta ttt atg ctg gct gca acg gcg gcg ttg ctt ttg aat			816
Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn			
260	265	270	
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Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly			
275	280	285	
ggc gcg gtg atg atg gcg tcc att att ttg gcg gca ggt acg ttt ttg			912
Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu			
290	295	300	
ggg att ttg aag ggt gcg ggg atg ttg gac gcg att tcc aaa gac att			960
Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Ile			
305	310	315	320
gtg cat atc ctg ccg gac gcg ctg ctg cct tat ctg cat att gcc atc			1008
Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile			
325	330	335	
ggt gtg ttg ggc att ccg ctt gag ttg gtt ttg agt acg gac gct tat			1056
Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr			
340	345	350	
tat ttc gga ctg ttt ccg att gtg gag cag att acc tcg cag gcg ggc			1104
Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly			
355	360	365	

gtg gcg ccc gaa gca.	gtt tat gcg atg ttg atc ggc ag	tc gtc	1152
Val Ala Pro Glu Ala	Gly Tyr Ala Met Leu Ile Gly Ser	Ile Val	
370	375	380	
ggc act ttt gtt acg ccg ctt tcg ccg gct ttg tgg atg ggc ttg ggt			1200
Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly			
385	390	395	400
ttg gcg aaa ttg tcg atg ggc aaa cac atc cgt tat tcg ttt ttt tgg			1248
Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp			
405	410	415	
gcg tgg ggt ttg tcg ctg gcg ata ttg gcc agt tcg ata gca gca gga			1296
Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly			
420	425	430	
atc gtg cct ctg ccg taa			1314
Ile Val Pro Leu Pro			
435			

<210> 12

<211> 437

<212> PRT

<213> Neisseria meningitidis

<400> 12

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Leu	Leu	Thr	Glu	Lys	Val	Ser	Pro	Ile	Ile	Ala	Leu	Ile	Leu	Val	Pro
				20				25				30			

Leu	Phe	Gly	Ala	Leu	Leu	Ala	Gly	Phe	Asp	Val	Ser	Gln	Leu	Lys	Glu
				35			40				45				

Phe	Tyr	Ser	Gly	Gly	Thr	Lys	Ser	Val	Met	Gln	Ile	Val	Ile	Met	Phe
					50		55		60						

Met	Phe	Ser	Ile	Leu	Phe	Phe	Gly	Ile	Met	Asn	Asp	Val	Gly	Leu	Phe
				65		70		75				80			

Arg	Pro	Met	Ile	Gly	Gly	Leu	Ile	Lys	Leu	Thr	Arg	Gly	Asn	Ile	Val
					85			90				95			

Ala	Val	Ser	Val	Gly	Thr	Val	Leu	Val	Ser	Val	Val	Ala	Gln	Leu	Asp
					100		105			110					

Gly	Ala	Gly	Ala	Thr	Thr	Phe	Leu	Leu	Val	Val	Pro	Ala	Leu	Leu	Pro
				115		120				125					

Leu	Tyr	Lys	Arg	Leu	His	Met	Asn	Pro	Tyr	Leu	Leu	Phe	Leu	Leu	Leu
				130		135			140						

Thr	Ser	Ser	Ala	Gly	Leu	Ile	Asn	Leu	Leu	Pro	Trp	Gly	Gly	Pro	Thr
					145		150		155		160				

Gly	Arg	Val	Ala	Ser	Val	Leu	Gly	Ala	Asp	Val	Gly	Glu	Leu	Tyr	Lys
					165			170			175				

Pro	Leu	Leu	Thr	Val	Gln	Ile	Ile	Gly	Val	Val	Phe	Ile	Leu	Ala	Leu
					180			185			190				

Ser	Leu	Leu	Leu	Gly	Val	Arg	Glu	Lys	Arg	Arg	Ile	Val	Arg	Glu	Leu
					195		200			205					

Gly Ala Leu Pro Ala Ile Ala Asp Leu Ile Lys Pro Val Phe Leu Ser  
 210 215 220

Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val  
 225 230 235 240

Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro  
 245 250 255

Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn  
 260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly  
 275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu  
 290 295 300

Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Ile  
 305 310 315 320

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile  
 325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr  
 340 345 350

Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly  
 355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val  
 370 375 380

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly  
 385 390 395 400

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp  
 405 410 415

Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly  
 420 425 430

Ile Val Pro Leu Pro  
 435

<210> 13  
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 <212> DNA  
 <213> Neisseria meningitidis

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 <222> (1)..(1152)

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 Met Gly Ile His Leu Asp Phe Gly Ile Ser Pro Lys Thr Phe Arg Gln  
 1 5 10 15

act tat ctg tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat 96  
 Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn  
 20 25 30

ctc gaa gcc gca tct tgt aaa tat atc aac gag ata tac caa cga gca		144
Leu Glu Ala Ala Ser. 35	Lys Tyr Ile Asn Glu Ile Tyr Glu Arg Ala	
	40	45
gac cca acc gca ccg ctg ttt cat ctg cgt aaa aaa ggc gca atc gtt		192
Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val		
50	55	60
cct aaa gaa gaa tac gtc gaa agt ttc gac gat ttg ggc aaa act cgc		240
Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg		
65	70	75
tac cgt ttt att aaa tcc gtt atc tac gaa cat atg aag aat ggt gcg		288
Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala		
85	90	95
tcg tta gtc tat aac cat att aac aac gag ccg ttt tca gac cat atc		336
Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile		
100	105	110
gcc cgt caa gtc gcc cgcc ttt gcc ggc gca cat act att gtt agt gga		384
Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly		
115	120	125
tat ctt gct ttt ggc agc gac gaa tct tat aaa aac cat tgg gat acc		432
Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr		
130	135	140
cgc gat gtg tat gcc atc cag ctt ttc ggc aag aaa cgt tgg caa ctt		480
Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu		
145	150	155
160		
act gcc cct gat ttc cct atg cca ttg tat atg caa cag act aaa gat		528
Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp		
165	170	175
act gat att tcc att cct gaa cat atc gat atg gat att atc ctt gaa		576
Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu		
180	185	190
gca ggt gat gtc ctc tac atc cca cgc ggt tgg tgg cac aga cct atc		624
Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile		
195	200	205
ccg ctc ggc tgt gaa acc ttc cac ttc gct gtc ggt acc ttc ccg ccc		672
Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro		
210	215	220
aac ggc tat aat tac ctc gag tgg cta atg aag aaa ttc ccc acg ata		720
Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile		
225	230	235
240		
gaa agt ctg cgc cac agt ttc tca gac tgg gag caa gat agg acg cgt		768
Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg		
245	250	255
atc aac gat act gcc gca caa att gct gcc atg att gcc gac ccc gtc		816
Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val		
260	265	270
aat tac gaa gcc ttc agt gaa gac ttc ctc ggc aaa gaa cgc acc gat		864
Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp		
275	280	285
acc gct ttt cat ctc gaa cag ttc gcg aat ccc aac gct act ccg ctt		912
Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu		

290

295

300

tca gac gac gtc agg	305	aga cta aat gcc aat aat ttg ga	310	cg ttg	960
Ser Asp Asp Val Arg		Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr		Leu	
	310		315		320
gaa aag gga tat ttg att ggg aat ggg atg aag ata agc gta gat gaa					1008
Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu					
	325		330		335
ttg ggg aaa aaa gtg tta gaa cac atc ggt aag aat gaa ccg tta ttg					1056
Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu					
	340		345		350
ttg aaa aat cta ctg gtt aac ttc aat cag gga aaa cat gaa gaa gtt					1104
Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val					
	355		360		365
agg aag ttg att tat cag ttg ata gag tta gat ttt ctg gaa ctt ttg					1152
Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Leu Leu					
	370		375		380
tga					1155

DRAFT - DO NOT CITE

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<211> 384					
<212> PRT					
<213> Neisseria meningitidis					
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Met Gly Ile His Leu Asp Phe Gly Ile Ser Pro Lys Thr Phe Arg Gln					
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Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn					
20		25		30	
Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala					
35		40		45	
Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val					
50		55		60	
Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg					
65		70		75	
Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala					
85		90		95	
Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile					
100		105		110	
Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly					
115		120		125	
Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr					
130		135		140	
Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu					
145		150		155	
160					
Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp					
165		170		175	
Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu					
180		185		190	

Ala Gly Asp Val Leu Ile Pro Arg Gly Trp Trp His Arg Pro Ile

195

200

205

Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro  
210 215 220

Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile  
225 230 235 240

Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg  
245 250 255

Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val  
260 265 270

Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp  
275 280 285

Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu  
290 295 300

Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu  
305 310 315 320

Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu  
325 330 335

Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu  
340 345 350

Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val  
355 360 365

Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Leu Leu  
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<212> DNA

<213> Neisseria meningitidis

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<222> (1)..(714)

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cgc caa acc agc ctg acg ggt aaa gtg att ctg aca cga ccg ttg tca 96  
Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser  
20 25 30

ttt tcc cta tgg acg aca ttt gca tcg ata tct gcg tta ttg att atc 144  
Phe Ser Leu Trp Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile  
35 40 45

ctg ttt ttg ata ttt ggt aac tat acg cga aag aca aca gtg gag gga 192  
Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Val Glu Gly  
50 55 60

caa att tta cct gca tcg ggc gta atc agg gtg tat gca ccg gat acg 240



Gly Asp Lys Leu Phe [REDACTED] Leu Ser Thr Ser Arg Phe Gly Ala [REDACTED] Asp  
 100 105 110

Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu  
 115 120 125

Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr  
 130 135 140

Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Lys Leu His  
 145 150 155 160

Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu  
 165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro  
 180 185 190

Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala  
 195 200 205

Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile  
 210 215 220

Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala  
 225 230 235

<210> 17

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<212> DNA

<213> Neisseria meningitidis

<220>

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<222> (1)...(687)

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gcc tac ggc cga gaa gaa gcc ggg ctg ctt cag gaa atc cgc acg cag  
 Ala Tyr Arg Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln  
 20 25 30

aat ctg aca ttg gcc agc ctc ccc aaa cgg cat gag aca gaa caa agc  
 Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser  
 35 40 45

cag ctt gaa cgc acc atg gcc gat att tct caa gaa gtt ttg gat ttt  
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe  
 50 55 60

gaa atg cgc tct gaa caa atc atc cgt gca gga cgg tcg ggt tat ata  
 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile  
 65 70 75 80

gca ata ccg aac gtc gaa gtc gga cag cag gtt gat cct tcc aaa ctg  
 Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu  
 85 90 95

ctc ttg agc att gtt ccc gaa cgt acc gag cta tat gcc cat cta tat

336

Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr  
 100 105 110  
 atc ccc agc agt gca gca ggc ttt atc aag ccg aaa gac aag gtt gtc 384  
 Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val  
 115 120 125  
 cta cgt tat cag gca tat ccc tat caa aaa ttc ggg ctt gct tcc ggc 432  
 Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly  
 130 135 140  
 agt gtc gta tca gta gca aaa acg gca ctg ggc aga cag gaa ttg tcg 480  
 Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser  
 145 150 155 160  
 gga ttg ggc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt 528  
 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val  
 165 170 175  
 tat ctc gtg aaa ata aaa ccc gac aaa cca acc atc act gca tac ggt 576  
 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly  
 180 185 190  
 gag gaa aaa ccg ctg caa atc ggc atg acg ttg gaa gca gac atc ctg 624  
 Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu  
 195 200 205  
 cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag ctg att tat agt 672  
 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser  
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 Met Ser Gly Lys Leu  
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 Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser  
 35 40 45  
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe  
 50 55 60  
 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile  
 65 70 75 80  
 Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu  
 85 90 95  
 Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr  
 100 105 110  
 Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val  
 115 120 125

Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly  
 130 . . . 135 140 .  
 Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser  
 145 150 155 160  
 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val  
 165 170 175  
 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly  
 180 185 190  
 Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu  
 195 200 205  
 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser  
 210 215 220  
 Met Ser Gly Lys Leu  
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Met	Lys	Phe	Phe	Pro	Ala	Pro	Cys	Leu	Leu	Val	Ile	Leu	Ala	Val	Ile		
1										10					15		
ccc	ctt	aaa	acc	tta	gct	gcc	gat	gaa	aac	gat	gca	gaa	ctt	atc	cgt		96
Pro	Leu	Lys	Thr	Leu	Ala	Ala	Asp	Glu	Asn	Asp	Ala	Glu	Leu	Ile	Arg		
										25					30		
tcc	atg	cag	cgt	cag	cag	cac	ata	gat	gct	gaa	ttg	tta	act	gat	gca		144
Ser	Met	Gln	Arg	Gln	Gln	His	Ile	Asp	Ala	Glu	Leu	Leu	Thr	Asp	Ala		
										40					45		
aat	gtc	cgt	ttc	gag	caa	cca	ttg	gag	aag	aac	aat	tat	gtc	ctg	agt		192
Asn	Val	Arg	Phe	Glu	Gln	Pro	Leu	Glu	Lys	Asn	Asn	Tyr	Val	Leu	Ser		
										50					60		
gaa	gat	gaa	aca	ccg	tgt	act	cg	gta	aat	tac	att	agt	tta	gat	gat		240
Glu	Asp	Glu	Thr	Pro	Cys	Thr	Arg	Val	Asn	Tyr	Ile	Ser	Leu	Asp	Asp		
										65					80		
aag	acg	gcg	cgc	aaa	ttt	tct	ttt	ctt	cct	tct	gtg	ctc	atg	aaa	gaa		288
Lys	Thr	Ala	Arg	Lys	Phe	Ser	Phe	Leu	Pro	Ser	Val	Leu	Met	Lys	Glu		
										85					95		
aca	gct	ttt	aaa	act	ggg	atg	tgt	tta	ggt	tcc	aat	aat	ttg	agc	agg		336
Thr	Ala	Phe	Lys	Thr	Gly	Met	Cys	Leu	Gly	Ser	Asn	Asn	Leu	Ser	Arg		
										100					110		
cta	caa	aaa	gcc	gcg	caa	cag	ata	ctg	att	gtg	cgt	ggc	tac	ctc	act		384
Leu	Gln	Lys	Ala	Ala	Gln	Gln	Ile	Leu	Ile	Val	Arg	Gly	Tyr	Leu	Thr		
										115					125		
tcc	caa	gct	att	atc	caa	cca	cag	aat	atg	gat	tcg	gga	att	ctg	aaa		432

Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys		
130 . . . . . 135	140	
tta cggtatcagtcgaaatcgaggatatccgcataatggaaa	480	
Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys		
145 150 155 160		
cgg gat gct aag tct gcc gag ggc agt att agt gca ttc aat aac aaa	528	
Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys		
165 170 175		
ctt ccc tta tat agg aac aaa att ctc aat ctt cgc gat gta gag cag	576	
Leu Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln		
180 185 190		
ggc ttg gaa aac ctg cgt ttg ccg agt gtt aaa aca gat att cag	624	
Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln		
195 200 205		
att ata ccg tcc gaa gaa gaa ggc aaa agc gat tta cag atc aaa tgg	672	
Ile Ile Pro Ser Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp		
210 215 220		
cag cag aat aaa ccc ata cgg ttc agt atc ggt ata gat gat gcg ggc	720	
Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly		
225 230 235 240		
ggc aaa acg acc ggc aaa tat caa gga aat gtc gct tta tcg tcc gat	768	
Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Ser Asp		
245 250 255		
aac cct ttg ggc tta agc gat tcg ttt tat gtt tca tat gga cgc ggt	816	
Asn Pro Leu Gly Leu Ser Asp Ser Phe Tyr Val Ser Tyr Gly Arg Gly		
260 265 270		
ttg gtg cac aaa acg gac ttg act gct gcc acc ggt acg gaa act gaa	864	
Leu Val His Lys Thr Asp Leu Thr Ala Ala Thr Gly Thr Glu Thr Glu		
275 280 285		
agc gga tcc aga agt tac agc gtg cat tat tcg gtg ccc gta aaa aaa	912	
Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys Lys		
290 295 300		
tgg ctg ttt tct ttt aat cac aat gga cat cgt tac cac gaa gca acc	960	
Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr		
305 310 315 320		
gaa ggc tat tcc gtc aat tac gat tac aac ggc aaa caa tat cag agc	1008	
Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser		
325 330 335		
agc ctg gcc gcc gag cgc atg ctt tgg ccc ccc agc ttt cct caa act	1056	
Ser Leu Ala Ala Glu Arg Met Leu Trp Pro Pro Ser Phe Pro Gln Thr		
340 345 350		
tca gtc cga atg aaa tta tgg aca cgc caa acc tat aaa tac atc gac	1104	
Ser Val Arg Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp		
355 360 365		
gat gcc gaa atc gaa gtg caa cgc cgc cgc tct gca ggc tgg gaa gcc	1152	
Asp Ala Glu Ile Glu Val Gln Arg Arg Ser Ala Gly Trp Glu Ala		
370 375 380		
gaa ttg cgc cac cgt gct tac ctc cac cgt tgg cag ctt gac ggc aag	1200	
Glu Leu Arg His Arg Ala Tyr Leu His Arg Trp Gln Leu Asp Gly Lys		
385 390 395 400		

ttg tct tac aaa cgc	acc ggc atg cgc caa agt atg	cct	1248
Leu Ser Tyr Lys Arg	Thr Gly Met Arg Gln Ser Met Pro	Ala Pro	
405	410	415	
gaa gaa aac ggc ggc ggt act att cca gcc aca tcc cgt atg aaa atc			1296
Glu Glu Asn Gly Gly Thr Ile Pro Ala Thr Ser Arg Met Lys Ile			
420	425	430	
ata acc gcc gga ttg gat gca gcg gcc ccg tct atg ttg ggc aaa cag			1344
Ile Thr Ala Gly Leu Asp Ala Ala Pro Ser Met Leu Gly Lys Gln			
435	440	445	
cag ttt ttc tac gca acc gcc att caa gct caa tgg aac aaa acg cct			1392
Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro			
450	455	460	
ttg gtt gcc caa gac aag ttg tct atc ggc agc cgc tac acc gtt cgc			1440
Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg			
465	470	475	480
gga ttt gat ggg gag cag agt ctt ttc gga gag cga ggt ttc tac tgg			1488
Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp			
485	490	495	
cag aat act tta act tgg tat ttt cat ccg aac cat cag ttc tat ctc			1536
Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu			
500	505	510	
ggt gcg gac tat ggc cgc gta tct ggc gaa agt gca caa tat gta tcg			1584
Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser			
515	520	525	
ggc aag cag ctg atg ggt gca gtg gtc ggc ttc aga gga ggg cat aaa			1632
Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys			
530	535	540	
gta ggc ggt atg ttt gct tat gat ctg ttt gcc ggc aag ccg ctt cat			1680
Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His			
545	550	555	560
aaa ccc aaa ggc ttt cag acg acc aac acc gtt tac ggc ttc aac ttg			1728
Lys Pro Lys Gly Phe Gln Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu			
565	570	575	
aat tac agt ttc taa			1743
Asn Tyr Ser Phe			
580			

<210> 20

<211> 580

<212> PRT

<213> Neisseria meningitidis

<400> 20

Met Lys Phe Phe Pro Ala Pro Cys Leu Leu Val Ile Leu Ala Val Ile			
1	5	10	15

Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg			
20	25	30	

Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala			
35	40	45	

Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser

50

55

60

Glu Asp Glu Thr Pro C [REDACTED] Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp  
 65 70 75 80

Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu  
 85 90 95

Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg  
 100 105 110

Leu Gln Lys Ala Ala Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr  
 115 120 125

Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys  
 130 135 140

Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys  
 145 150 155 160

Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys  
 165 170 175

Leu Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln  
 180 185 190

Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln  
 195 200 205

Ile Ile Pro Ser Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp  
 210 215 220

Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly  
 225 230 235 240

Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Ser Asp  
 245 250 255

Asn Pro Leu Gly Leu Ser Asp Ser Phe Tyr Val Ser Tyr Gly Arg Gly  
 260 265 270

Leu Val His Lys Thr Asp Leu Thr Ala Ala Thr Gly Thr Glu Thr Glu  
 275 280 285

Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys Lys  
 290 295 300

Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr  
 305 310 315 320

Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser  
 325 330 335

Ser Leu Ala Ala Glu Arg Met Leu Trp Pro Pro Ser Phe Pro Gln Thr  
 340 345 350

Ser Val Arg Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp  
 355 360 365

Asp Ala Glu Ile Glu Val Gln Arg Arg Arg Ser Ala Gly Trp Glu Ala  
 370 375 380

Glu Leu Arg His Arg Ala Tyr Leu His Arg Trp Gln Leu Asp Gly Lys  
 385 390 395 400

Leu Ser Tyr Lys Arg Gly Thr Gly Met Arg Gln Ser Met Pro Ala Pro

405	410	415
Glu Glu Asn Gly Gly	Thr Ile Pro Ala Thr Ser Arg Met Lys Ile	
420	425	430
Ile Thr Ala Gly Leu Asp Ala Ala Ala Pro Ser Met Leu Gly Lys Gln		
435	440	445
Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro		
450	455	460
Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg		
465	470	480
Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp		
485	490	495
Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu		
500	505	510
Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser		
515	520	525
Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys		
530	535	540
Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His		
545	550	560
Lys Pro Lys Gly Phe Gln Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu		
565	570	575
Asn Tyr Ser Phe		
580		

<210> 21  
 <211> 411  
 <212> DNA  
 <213> Neisseria meningitidis

<220>  
 <221> CDS  
 <222> (1)...(408)

<400> 21						
atg att gaa ttt gtc cga gcc aaa aaa cgg ctg ctt tgg gca ttt gtg						48
Met Ile Glu Phe Val Arg Ala Lys Lys Arg Leu Leu Trp Ala Phe Val						
1	5	10			15	
ctt ttg ctt gtg tgg acg tgc ggt tac cga tac gac aag gcc						96
Leu Leu Leu Val Trp Thr Cys Gly Tyr Arg Ala Ala Asp Lys Ala						
20	25	30				
gaa gcg aaa caa acc gcc ctg att gcc acc tat cgg cat tct tct atg						144
Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met						
35	40	45				
gtt gcg gcg gaa caa tac gcc ttg cag ctt aaa aaa gcg cag gac gaa						192
Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu						
50	55	60				
agg cag cgg tgg tac gac ttt tcc caa aaa caa gga aga aag ccc gtg						240
Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val						
65	70	75			80	

aaa aaa cag tat ccg [REDACTED] caa acg aaa aaa gcc ggc tat c [REDACTED] aa acc 288  
Lys Lys Gln Tyr Pro [REDACTED] Gln Thr Lys Lys Ala Gly Tyr Le [REDACTED] Lys Thr  
85 90 95

aag gaa gaa ctg ctt gcg gaa ttg gct tgc ctt aaa gcg gaa atg gct 336  
Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala  
100 105 110

gcc cta aaa aag ctc gat gcc tta atc tat ggg aaa gaa gtg cgg cag 384  
Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln  
115 120 125

aaa gaa cgc aac tcg tcg cag ggt taa 411  
Lys Glu Arg Asn Ser Ser Gln Gly  
130 135

<210> 22

<211> 136

<212> PRT

<213> Neisseria meningitidis

<400> 22

Met Ile Glu Phe Val Arg Ala Lys Lys Arg Leu Leu Trp Ala Phe Val  
1 5 10 15

Leu Leu Leu Val Trp Thr Cys Gly Tyr Arg Tyr Ala Ala Asp Lys Ala  
20 25 30

Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met  
35 40 45

Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu  
50 55 60

Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val  
65 70 75 80

Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr  
85 90 95

Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala  
100 105 110

Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln  
115 120 125

Lys Glu Arg Asn Ser Ser Gln Gly  
130 135

<210> 23

<211> 924

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(921)

<400> 23

atg caa tac agc aca ctg gca gga caa acc gac aac tcc ctc gtt tcc 48  
Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser  
1 5 10 15

aat aat ttc ggg ttt,   cgc ctg ccg ctt aat ttt atg cc   t gaa		96	
Asn Asn Phe Gly Phe Ile Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu			
20	25	30	
agt cat gcc gat tgg gtt att acc ggc gtg cct tat gat atg gcg gtt		144	
Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val			
35	40	45	
tca ggg cgt tcc ggc gcg cgt ttc ggt cct gaa gcc atc cg <sup>g</sup> cgc gcc		192	
Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala			
50	55	60	
tcc gtc aac ctc gct tgg gag cac cgc agg ttt cca tgg aca ttt gat		240	
Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp			
65	70	75	80
gtg cgc gaa cgc ctg aac att att gat tgc ggc gac ttg gtt ttt tct		288	
Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser			
85	90	95	
ttt ggc gac agc agg gat ttt gtc gaa aaa atg gaa gcg cac gcc ggc		336	
Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly			
100	105	110	
aaa tta ctt tct tcc ggc aaa cgc tgt ttg agt ttg ggc ggc gac cat		384	
Lys Leu Ser Ser Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His			
115	120	125	
ttc att acc ctc ccg ttg ttg cgc gcc cac gcc cgc tat ttc ggc aaa		432	
Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys			
130	135	140	
ctc gca ctg att cat ttt gac gcg cac acc gac acc tac gac aac ggc		480	
Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly			
145	150	155	160
- agc gaa tac gac cac ggt acg atg ttc tat acc gcc ccc aag gaa ggc		528	
Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly			
165	170	175	
ctc atc gac ccg tcc cgt tcc gta caa atc ggc ata cgt acc gaa cac		576	
Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His			
180	185	190	
agt aaa aaa ttg cct ttt act gtg ttg acc gcc ccc caa gtt aat gaa		624	
Ser Lys Lys Leu Pro Phe Thr Val Leu Thr Ala Pro Gln Val Asn Glu			
195	200	205	
gac agt gtt gaa gag acc gtc cgt aaa atc aaa gaa acc gtc ggc aat		672	
Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn			
210	215	220	
atg ccc gtt tac ctg act ttc gac ata gac tgc ctc gac ccg tcg ttc		720	
Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe			
225	230	235	240
gcc ccc ggg acc ggt acg ccc gta tgc ggc ggc ttg agc agc gac agg		768	
Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg			
245	250	255	
gca tta aaa atc cta cgt ggg ctg acg gat ctc gac atc gtc ggt atg		816	
Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met			
260	265	270	
gat gtt gta gaa gtt gcc ccc tct tac gac caa tcc gac att acc gct		864	

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala			
275 . .	280	285	
ttg gcc ggc gcc aca att gcc ttg gaa atg ctt tac ctt caa ggt gcg		912	
Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala			
290	295	300	
aaa aag gac tga		924	
Lys Lys Asp			
305			
<210> 24			
<211> 307			
<212> PRT			
<213> Neisseria meningitidis			
<400> 24			
Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser			
1	5	10	15
Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu			
20	25	30	
Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val			
35	40	45	
Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala			
50	55	60	
Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp			
65	70	75	80
Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser			
85	90	95	
Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly			
100	105	110	
Lys Leu Leu Ser Ser Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His			
115	120	125	
Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys			
130	135	140	
Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly			
145	150	155	160
Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly			
165	170	175	
Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His			
180	185	190	
Ser Lys Lys Leu Pro Phe Thr Val Leu Thr Ala Pro Gln Val Asn Glu			
195	200	205	
Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn			
210	215	220	
Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe			
225	230	235	240
Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg			
245	250	255	

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met  
 260. 265 270

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala  
 275 280 285

Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala  
 290 295 300

Lys Lys Asp  
 305

<210> 25  
 <211> 426  
 <212> DNA  
 <213> Neisseria meningitidis

<220>  
 <221> CDS  
 <222> (1)...(423)

<400> 25

atg gag cag tcg ggc aaa ttc agt tgg tct gcg gca gct ttt tgg gac	48
Met Glu Gln Ser Gly Lys Phe Ser Trp Ser Ala Ala Ala Phe Trp Asp	
1 5 10 15	

att ccc tac ccc gtc acc agg cgg att gcc tca agt ttg tat tcg acc 96

Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr	
20 25 30	

gaa tat ttt gtc gta tgc ttt ctg cgt ttg atg cca ctc tct ccg tgt 144

Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys	
35 40 45	

aat ctg tat ttt gtc acc cat ctg cgt acc aat gaa tcg gaa ata gaa 192

Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu	
50 55 60	

aga tgg tct gct gtt ccc tgc caa ata gta ttg aac gac ggc aag tcg 240

Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser	
65 70 75 80	

gaa ttc ggc gga ttc gca ttt gaa gtg caa ctt tcc cta aca gaa aaa 288

Glu Phe Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys	
85 90 95	

ggc cag tat gcg gta gca tac gac ctt tcc tgc aag aaa gat tgc cat 336

Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His	
100 105 110	

gag cta cac gca act gac cca agg cga acg ata cca cat cca ata cct 384

Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro	
115 120 125	

gtc ccg cca ctg cac cgt cac cga aat cgc caa aca gct taa 426

Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala	
130 135 140	

<210> 26  
 <211> 141  
 <212> PRT  
 <213> Neisseria meningitidis

<400> 26  
 Met Glu Gln Ser Gly Ile Phe Ser Trp Ser Ala Ala Ala Phe Asp  
 1 5 10 15

Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr  
 20 25 30

Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys  
 35 40 45

Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu  
 50 55 60

Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser  
 65 70 75 80

Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys  
 85 90 95

Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His  
 100 105 110

Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro  
 115 120 125

Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala  
 130 135 140

400-360  
 <210> 27  
 <211> 351  
 <212> DNA  
 <213> Neisseria meningitidis

<220>  
 <221> CDS  
 <222> (1)...(348)

<400> 27  
 atg caa aac ggc ggg gga aag att tac cag acg gcg gac aat gtg gaa 48  
 Met Gln Asn Gly Gly Lys Ile Tyr Gln Thr Ala Asp Asn Val Glu  
 1 5 10 15

ggg att atg ctg ttg aag gta gta cct gag cgt acc gtt tcg gca gat 96  
 Gly Ile Met Leu Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp  
 20 25 30

gca aaa acc aga gac ccg atg tgg gac aat gcg gct tta cag acc agc 144  
 Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser  
 35 40 45

gaa ggc gta aat ttt att gct cgt ttc cta gga ttt ttt agc gat ggg 192  
 Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly  
 50 55 60

gaa tac cgc tat gtg gat gtc ctg caa ccc aac cat tcc gat att att 240  
 Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile  
 65 70 75 80

cggtat tca ggt aaa gat ttt ccg cta aat caa ata ctt aac cat ata 288  
 Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile  
 85 90 95

cac ccc gcc cgt tat gcg gta acg ttc gaa aac aat gtc gat tcc aag 336  
 His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys

100

105

110

351

ctg cgc agg cac tga  
 Leu Arg Arg His  
 115

<210> 28  
<211> 116  
<212> PRT  
<213> Neisseria meningitidis

<400> 28  
 Met Gln Asn Gly Gly Lys Ile Tyr Gln Thr Ala Asp Asn Val Glu  
 1 5 10 15  
 Gly Ile Met Leu Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp  
 20 25 30  
 Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser  
 35 40 45  
 Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly  
 50 55 60  
 Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile  
 65 70 75 80  
 Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile  
 85 90 95  
 His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys  
 100 105 110  
 Leu Arg Arg His  
 115

<210> 29  
<211> 1404  
<212> DNA  
<213> Neisseria meningitidis

<220>  
<221> CDS  
<222> (1)..(1401)

<400> 29  
 atg aca ttg ctc aat cta atg ata atg caa gat tac ggt att tcc gtt 48  
 Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val  
 1 5 10 15  
 tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tcg gct atg 96  
 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met  
 20 25 30  
 aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144  
 Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu  
 35 40 45  
 cca cta tcc ctt tcc cca tcc gtt tcg gct ttt acg ctg cct gaa gca 192  
 Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala  
 50 55 60  
 tgg cgG gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac 240



gtc ggc gta cag ttg a	ttg ccg ctt tat acc ggc gga gaa	tcg	1056
Val Gly Val Gln Leu A	Leu Pro Leu Tyr Thr Gly Gly Glu	Leu Ser	
340	345	350	
ggc aaa atc cat gaa gcc gaa gcg caa tac ggg gcc gaa gca cag			1104
Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln			
355	360	365	
ctg acc gca acc gag cg <sup>g</sup> cac atc aaa ctc gcc gta cgc cag gct tat			1152
Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr			
370	375	380	
acc gaa agc ggt gc <sup>g</sup> gc <sup>g</sup> cgt tac caa atc atg gc <sup>g</sup> caa gaa cg <sup>g</sup> gtt			1200
Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val			
385	390	395	400
ttg gaa agc agc cgt ttg aaa ctg aaa tcg acc gaa acc ggc caa caa			1248
Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln			
405	410	415	
tac ggc atc cgc aac cg <sup>g</sup> ctg gaa gta ata cg <sup>g</sup> gc <sup>g</sup> cg <sup>g</sup> cag gaa gtc			1296
Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val			
420	425	430	
gcc caa gca gaa cag aaa ctg gct caa gca cg <sup>g</sup> tat aaa ttc atg ctg			1344
Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu			
435	440	445	
gct tat ttg cgc ttg gtg aaa gag agc ggg tta ggg ttg gaa acg gta			1392
Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val			
450	455	460	
ttt gc <sup>g</sup> gaa taa			1404
Phe Ala Glu			
465			
<210> 30			
<211> 467			
<212> PRT			
<213> Neisseria meningitidis			
<400> 30			
Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val			
1	5	10	15
Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met			
20	25	30	
Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu			
35	40	45	
Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala			
50	55	60	
Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr			
65	70	75	80
Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe			
85	90	95	
Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser			
100	105	110	
Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln			

115

120

125

Thr Leu Phe Asp Ala A Lys Phe Ala Gln Tyr Arg Gln Ser Phe  
 130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu  
 145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp  
 165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val  
 180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp  
 195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile  
 210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr  
 225 230 235 240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu  
 245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp  
 260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu  
 275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg  
 290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr  
 305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser  
 325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser  
 340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln  
 355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr  
 370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val  
 385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln  
 405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val  
 420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu  
 435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val  
 450 455 460

Phe Ala Glu

<210> 31  
<211> 696  
<212> DNA  
<213> *Neisseria meningitidis*

<220>  
<221> CDS  
<222> (1)..(693)

<400> 31  
 atg aaa caa tcc gcc cga ata aaa aat atg gat cag aca tta aaa aat 48  
 Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn  
 1 5 10 15  
  
 aca ttg ggc att tgc gcg ctt tta gcc ttt tgt ttt ggc gcg gcc atc 96  
 Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile  
 20 25 30  
  
 gca tca ggt tat cac ttg gaa tat gaa tac ggc tac cgt tat tct gcc 144  
 Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala  
 35 40 45  
  
 gtg ggt gct ttg gct tcg gtt gta ttt tta tta ttg gca cgc ggt 192  
 Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly  
 50 55 60  
  
 ttc ccg cgc gtt tct tca gtt gtt tta ctg att tac gtc ggc aca acc 240  
 Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr  
 65 70 75 80  
  
 gcc cta tat ttg ccg gtc ggc tgg ctg tat ggt gcg ccg tct tat cag 288  
 Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln  
 85 90 95  
  
 ata gtc ggt tcg ata ttg gaa agc aat cct gcc gag gcg cgt gaa ttt 336  
 Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe  
 100 105 110  
  
 gtc ggc aat ctt ccc ggg tcg ctt tat ttt gtg cag gca tta ttt ttc 384  
 Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe  
 115 120 125  
  
 att ttt ggc ttg aca gtt tgg aga tat tgt gta tcg ggg ggg gta ttt 432  
 Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe  
 130 135 140  
  
 gct gac gta aaa aac tat aaa cgc cgc agc aaa ata tgg ctg act ata 480  
 Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile  
 145 150 155 160  
  
 tta ttg act ttg att ttg tcc tgc gcg gtg atg gat aaa atc gcc agc 528  
 Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser  
 165 170 175  
  
 gat aaa gat ttg cga gaa cct gat gcc ggc ctg ttg ttg aat att ttc 576  
 Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe  
 180 185 190  
  
 gac ctg tat tac gat ttg gct tcc gcg ccg gca cca ata tgt cgc caa 624  
 Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln  
 195 200 205

gcu ggc cca cat ttt gga agc agc aaa aaa agc gtc aac atg cca tat 672  
Ala Arg Pro His Phe, C Ser Ser Lys Lys Ser Val Asn Met Tyr  
210 215 220

ccg tca tgt tgc gcc caa gta taa 696  
Pro Ser Cys Cys Ala Gln Val  
225 230

<210> 32  
<211> 231  
<212> PRT  
<213> Neisseria meningitidis

<400> 32  
Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn  
1 5 10 15

Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile  
20 25 30

Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala  
35 40 45

Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly  
50 55 60

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr  
65 70 75 80

Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln  
85 90 95

Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe  
100 105 110

Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe  
115 120 125

Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe  
130 135 140

Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile  
145 150 155 160

Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser  
165 170 175

Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe  
180 185 190

Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln  
195 200 205

Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr  
210 215 220

Pro Ser Cys Cys Ala Gln Val  
225 230

<210> 33  
<211> 909  
<212> DNA  
<213> Neisseria meningitidis

<220>  
<221> CDS  
<222> (1)..(906)

<400> 33  
atg aat gtt tac ggt ttc cca ttg ccc gat acg cct ttt ttg agt cg<sup>48</sup>  
Met Asn Val Tyr Gly Phe Pro Leu Pro Asp Thr Pro Phe Leu Ser Arg  
1 5 10 15

acc aaa ggg ctg ttg ata aac ggt tac cat tt<sup>c</sup> acc gcc cac gc<sup>96</sup>  
Thr Lys Gly Leu Leu Ile Asn Gly Tyr His Phe Thr Ala His Ala Thr  
20 25 30

aat ctt tcg ctg ccg cag act ttg ggg ctg ccg gga gag ccg aac aat  
Asn Leu Ser Leu Pro Gln Thr Leu Gly Leu Pro Gly Glu Pro Asn Asn  
35 40 45

aac att gtc agc ttg gc<sup>192</sup> g aag cag gc<sup>50</sup> g ggt tt<sup>c</sup> gg<sup>55</sup> acg gc<sup>60</sup> gg<sup>c</sup> ctg  
Asn Ile Val Ser Leu Ala Lys Gln Ala Gly Phe Arg Thr Ala Trp Leu

tct aat caa gga atg ttg ggg cat tt<sup>c</sup> gcc aac gaa att tcc acc tat  
Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr  
65 70 75 80

gcc cta cgc agc gat tat ccg tgg tt<sup>c</sup> acc caa agg ggt gat tat ggc  
Ala Leu Arg Ser Asp Tyr Pro Trp Phe Thr Gln Arg Gly Asp Tyr Gly  
85 90 95

aaa agc gc<sup>336</sup> g ggg ttg agc gac cgc ctt ttg ccg gc<sup>100</sup> ttc aaa cg<sup>105</sup> g  
Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Leu Pro Ala Phe Lys Arg  
100 105 110

gtt ttg ata gga aat gca ggc acg aag cct ccg ctg att gtg atg cac  
Val Leu Ile Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His  
115 120 125

ctg atg ggt tcg cac agt gat tt<sup>c</sup> tgc aca cgt ttg gat aag gat gc<sup>432</sup>  
Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala  
130 135 140

cg<sup>480</sup> gg ttt cag tat caa act gaa aaa ata tcc tgc tat gtt tcc acc  
Arg Arg Phe Gln Tyr Gln Thr Glu Lys Ile Ser Cys Tyr Val Ser Thr  
145 150 155 160

atc gc<sup>528</sup> g caa acc gat aaa tt<sup>c</sup> tta gaa gat aca gtt aag ata ttg aat  
Ile Ala Gln Thr Asp Lys Phe Leu Glu Asp Thr Val Lys Ile Leu Asn  
165 170 175

gaa aat aaa gaa agc tgg tct ttg gtt tac tt<sup>c</sup> tcc gac cac ggt ttg  
Glu Asn Lys Glu Ser Trp Ser Leu Val Tyr Phe Ser Asp His Gly Leu  
180 185 190

atg cat gtc ggt aaa ggc ggc gag cga acg ttg aca cat ggt gc<sup>624</sup> g tgg  
Met His Val Gly Lys Gly Glu Arg Thr Leu Thr His Gly Ala Trp  
195 200 205

aag cgt caa agc tac ggc gtg ccg ctg gtt aaa att tcg tcc gat gac  
Lys Arg Gln Ser Tyr Gly Val Pro Leu Val Lys Ile Ser Ser Asp Asp  
210 215 220

acg cg<sup>720</sup> gg cgc gaa atg att aaa gtg agg cgc acg gc<sup>225</sup> g ttt aat tt<sup>c</sup> tta  
Thr Arg Arg Glu Met Ile Lys Val Arg Arg Ser Ala Phe Asn Phe Leu  
230 235 240

cgc gga ttc ggc agt tgg acg ggt atc gaa acc gac gag ttg cc gat 768  
Arg Gly Phe Gly Ser. Thr Thr Gly Ile Glu Thr Asp Glu Leu Asp  
245 250 255

gac ggc tat gat ttt tgg ggg aat gtt ccc gat gtg cag ggc gaa ggc 816  
Asp Gly Tyr Asp Phe Trp Gly Asn Val Pro Asp Val Gln Gly Glu Gly  
260 265 270

aat aac ctt gcc ttt atc gac gga ctg ccc gac gac ccc gcg ccg tgg 864  
Asn Asn Leu Ala Phe Ile Asp Gly Leu Pro Asp Asp Pro Ala Pro Trp  
275 280 285

tat gcg gga aaa ggc aaa tcg act aaa aat acg tct aaa aaa tga 909  
Tyr Ala Gly Lys Gly Lys Ser Thr Lys Asn Thr Ser Lys Lys  
290 295 300

<210> 34

<211> 302

<212> PRT

<213> Neisseria meningitidis

<400> 34

Met Asn Val Tyr Gly Phe Pro Leu Pro Asp Thr Pro Phe Leu Ser Arg  
1 5 10 15

Thr Lys Gly Leu Leu Ile Asn Gly Tyr His Phe Thr Ala His Ala Thr  
20 25 30

Asn Leu Ser Leu Pro Gln Thr Leu Gly Leu Pro Gly Glu Pro Asn Asn  
35 40 45

Asn Ile Val Ser Leu Ala Lys Gln Ala Gly Phe Arg Thr Ala Trp Leu  
50 55 60

Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr  
65 70 75 80

Ala Leu Arg Ser Asp Tyr Pro Trp Phe Thr Gln Arg Gly Asp Tyr Gly  
85 90 95

Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Leu Pro Ala Phe Lys Arg  
100 105 110

Val Leu Ile Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His  
115 120 125

Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala  
130 135 140

Arg Arg Phe Gln Tyr Gln Thr Glu Lys Ile Ser Cys Tyr Val Ser Thr  
145 150 155 160

Ile Ala Gln Thr Asp Lys Phe Leu Glu Asp Thr Val Lys Ile Leu Asn  
165 170 175

Glu Asn Lys Glu Ser Trp Ser Leu Val Tyr Phe Ser Asp His Gly Leu  
180 185 190

Met His Val Gly Lys Gly Glu Arg Thr Leu Thr His Gly Ala Trp  
195 200 205

Lys Arg Gln Ser Tyr Gly Val Pro Leu Val Lys Ile Ser Ser Asp Asp  
210 215 220

Thr Arg Arg Glu Met Ile Lys Val Arg Arg Ser Ala Phe Asn Phe Leu

225

230

235

240

Arg Gly Phe Gly Ser Thr Gly Ile Glu Thr Asp Glu Leu Pro Asp  
 245 250 255

Asp Gly Tyr Asp Phe Trp Gly Asn Val Pro Asp Val Gln Gly Glu Gly  
 260 265 270

Asn Asn Leu Ala Phe Ile Asp Gly Leu Pro Asp Asp Pro Ala Pro Trp  
 275 280 285

Tyr Ala Gly Lys Gly Lys Ser Thr Lys Asn Thr Ser Lys Lys  
 290 295 300

&lt;210&gt; 35

&lt;211&gt; 864

&lt;212&gt; DNA

&lt;213&gt; Neisseria meningitidis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(861)

&lt;400&gt; 35

atg atg agt caa cac tct gcc gga gca cgt ttc cgc caa gcc gtg aaa	48
Met Met Ser Gln His Ser Ala Gly Ala Arg Phe Arg Gln Ala Val Lys	
1 5 10 15	

gaa tcg aat ccg ctt gcc gtc gcc ggt tgc gtc aat gct tat ttt gca	96
Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala	
20 25 30	

cga ttg gcc acc caa agc ggt ttc aaa gcc atc tat ctg tcc ggc ggc	144
Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly	
35 40 45	

ggc gtg gca gcc tgt tct tgc ggt atc cct gat ttg ggc att acc aca	192
Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr	
50 55 60	

atg gaa gat gtg ctg atc gac gca cga cgc att acg gac aac gtg gat	240
Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp	
65 70 75 80	

acg cct ctg ctg gtg gac atc gat gtg ggt tgg ggc ggt gca ttc aat	288
Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn	
85 90 95	

att gcc cgt acc att cgc aac ttt gaa cgc gcc ggt gtt gca gcg gtt	336
Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val	
100 105 110	

cac atc gaa gat cag gta gcg caa aaa cgc tgc ggc cac cgt ccg aac	384
His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn	
115 120 125	

aaa gcc att gta tct aaa gat gaa atg gtc gac cgt atc aaa gct gcc	432
Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala	
130 135 140	

gta gat gcg cgc gtt gat gag aac ttc gtg att atg gcg cgt acc gat	480
Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp	
145 150 155 160	

gct gtc gaa gat ttg gat gcc gct atc gaa cgc gcc aa gct 528  
Ala Leu Ala Val Glu Cys Leu Asp Ala Ala Ile Glu Arg Ala Ala  
165 170 175

tgt gtc gaa gcc ggt gcg gac atg att ttc cct gaa gcc atg acc gat 576  
Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Glu Ala Met Thr Asp  
180 185 190

ttg aac atg tac cgc caa ttt gca gat gct gtg aaa gtg ccc gtg ttg 624  
Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu  
195 200 205

gct aac att acc gag ttt ggt tcc act ccg ctt tat acc caa agc gag 672  
Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu  
210 215 220

ctg gct gaa aac ggc gtg tcg ctg gtg ctg tat ccg ctg tca tcg ttc 720  
Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe  
225 230 235 240

cgt gca gca agc aaa gcc gct ctg aat gtt tac gaa gcc att atg cgc 768  
Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg  
245 250 255

gat ggc act tca ggc ggc ggt ggt gga cag tat gca aac ccg tgc cga 816  
Asp Gly Thr Ser Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg  
260 265 270

gct gta cga gca tct gaa cta tca tgc ctt cga gca aaa act gga taa 864  
Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly  
275 280 285

<210> 36

<211> 287

<212> PRT

<213> Neisseria meningitidis

<400> 36

Met Met Ser Gln His Ser Ala Gly Ala Arg Phe Arg Gln Ala Val Lys  
1 5 10 15

Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala  
20 25 30

Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly  
35 40 45

Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr  
50 55 60

Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp  
65 70 75 80

Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn  
85 90 95

Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val  
100 105 110

His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn  
115 120 125

Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala  
130 135 140

Val Asp Ala Arg Val Asn Glu Asn Phe Val Ile Met Ala Arg Thr Asp  
 145 . . . . . 155 160  
 Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala  
 165 170 175  
 Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Glu Ala Met Thr Asp  
 180 185 190  
 Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu  
 195 200 205  
 Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu  
 210 215 220  
 Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe  
 225 230 235 240  
 Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg  
 245 250 255  
 Asp Gly Thr Ser Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg  
 260 265 270  
 Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly  
 275 280 285

LOCUS 220860

<210> 37  
 <211> 921  
 <212> DNA  
 <213> Neisseria meningitidis  
  
 <220>  
 <221> CDS  
 <222> (1)..(918)  
  
 <400> 37  
 atg cct tcg agc aaa aac tgg ata aat tgt ttc aaa aat gat tta ccg 48  
 Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro  
 1 5 10 15  
  
 ctt tca gac tgc ctt tca aca aat ccg cat cggtcg tct gaa aac ccg 96  
 Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro  
 20 25 30  
  
 aaa ccc ata aaa aca caa agg aga aat acc atg act gaa act act caa 144  
 Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln  
 35 40 45  
  
 acc ccg acc ctc aaa cct aaa aaa tcc gtt gcg ctt tct ggc gtt gcg 192  
 Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala  
 50 55 60  
  
 gcc ggt aat acc gct ttg tgt acc gtt ggc cgt acc ggc aac gat ttg 240  
 Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu  
 65 70 75 80  
  
 agc tat cgc ggt tac gac att ctg gat ttg gca caa aaa tgt gag ttt 288  
 Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe  
 85 90 95  
  
 gaa gaa gtt gcc cac ctg ctg att cac ggc cat tta ccc aac aaa ttc 336  
 Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe  
 100 105 110

gag ctg gcc gct tat, a	gcc aag ctc aaa tcc atg cgc ggc g	cct	384
Glu Leu Ala Ala Tyr Lys Ala	Lys Leu Lys Ser Met Arg Gly Leu Pro		
115	120	125	
atc cgt gtg att aaa gtt ttg gaa agc ctg cct gca cat acc cat ccg	Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro		432
130	135	140	
atg gac gtg atg cgt acc ggc gta tcc atg ctg ggc tgt gtt cat cct	Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro		480
145	150	155	160
gaa cgt gaa ggc cat ccg gaa agc gaa gcg cgc gac att gcc gac aaa	Glu Arg Glu Gly His Pro Glu Ser Glu Ala Arg Asp Ile Ala Asp Lys		528
165	170	175	
ctg atc gcc agc ctc ggc agt atc ctc ttg tac tgg tat caa tat tcg	Leu Ile Ala Ser Leu Gly Ser Ile Leu Leu Tyr Trp Tyr Gln Tyr Ser		576
180	185	190	
cac aac ggc aaa cgcc att gaa gtt gaa agc gaa gaa gag acc atc ggc	His Asn Gly Lys Arg Ile Glu Val Glu Ser Glu Glu Thr Ile Gly		624
195	200	205	
ggt cat ttc ctg cac ctg ttg cac ggc aaa cgcc cca agc gaa tca cac	Gly His Phe Leu His Leu His Gly Lys Arg Pro Ser Glu Ser His		672
210	215	220	
atc aaa gcc atg cac gtt tca ctg att ctg tat gcc gaa cac gag ttc	Ile Lys Ala Met His Val Ser Leu Ile Leu Tyr Ala Glu His Glu Phe		720
225	230	235	240
aac gct tct acc ttt acc gcc cgcc gtg atc gcc ggt aca ggc tct gat	Asn Ala Ser Thr Phe Thr Ala Arg Val Ile Ala Gly Thr Gly Ser Asp		768
245	250	255	
atg tac tcc agc att acc gga gca atc ggc gcg ttg aaa ggt ccg aaa	Met Tyr Ser Ser Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Lys		816
260	265	270	
cac ggc ggc gcg aac gaa ggg ctt acg ata ttc aaa aac gct acc gca	His Gly Gly Ala Asn Glu Gly Leu Thr Ile Phe Lys Asn Ala Thr Ala		864
275	280	285	
atg ccg acg aag ccg aag ccg aca tcc gcg aac gca tcg gcc gca aag	Met Pro Thr Lys Pro Lys Pro Thr Ser Ala Asn Ala Ser Ala Ala Lys		912
290	295	300	
aaa tcg tga			921
Lys Ser			
305			

<210> 38  
<211> 306  
<212> PRT  
<213> Neisseria meningitidis

<400> 38  
Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro  
1 5 10 15  
Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro  
20 25 30

Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln  
35 . . 40 45

Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala  
50 55 60

Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu  
65 70 75 80

Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe  
85 90 95

Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe  
100 105 110

Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro  
115 120 125

Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro  
130 135 140

Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro  
145 150 155 160

Glu Arg Glu Gly His Pro Glu Ser Glu Ala Arg Asp Ile Ala Asp Lys  
165 170 175

Leu Ile Ala Ser Leu Gly Ser Ile Leu Leu Tyr Trp Tyr Gln Tyr Ser  
180 185 190

His Asn Gly Lys Arg Ile Glu Val Glu Ser Glu Glu Glu Thr Ile Gly  
195 200 205

Gly His Phe Leu His Leu Leu His Gly Lys Arg Pro Ser Glu Ser His  
210 215 220

Ile Lys Ala Met His Val Ser Leu Ile Leu Tyr Ala Glu His Glu Phe  
225 230 235 240

Asn Ala Ser Thr Phe Thr Ala Arg Val Ile Ala Gly Thr Gly Ser Asp  
245 250 255

Met Tyr Ser Ser Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Lys  
260 265 270

His Gly Gly Ala Asn Glu Gly Leu Thr Ile Phe Lys Asn Ala Thr Ala  
275 280 285

Met Pro Thr Lys Pro Lys Pro Thr Ser Ala Asn Ala Ser Ala Ala Lys  
290 295 300

Lys Ser  
305

<210> 39  
<211> 945  
<212> DNA  
<213> Neisseria meningitidis

<220>  
<221> CDS  
<222> (1)...(942)

<400> 39

PDB ID: 1E6D

atg cac cta tgt gga aag tat tat gga gta aat atg aag ctc gat Met His Leu Cys Gly Tyr Tyr Gly Val Asn Met Lys Leu Asp	48
1 5 10 15	
tta ctg atg gga ata ttc ttg gca gtt tct gcg gcc ctt ctg aat gca Leu Leu Met Gly Ile Phe Leu Ala Val Ser Ala Ala Leu Leu Asn Ala	96
20 25 30	
acc atc ggc ata ttc agc aag ata ttg atg gag cag ggc ttg tct gtt Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val	144
35 40 45	
cag cat att gca ttt ttg aaa act ttg aca ggt ttc gtg ttt atc agc Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser	192
50 55 60	
att ttg ctt tgc cgt acc ggt ttt acc aga cag att gcg gat att tca Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser	240
65 70 75 80	
aga aag aaa gag gca att ttg ccg ttg ctg tta aaa gta gca att tgt Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Lys Val Ala Ile Cys	288
85 90 95	
gct ttt ttc gga att tat acg ttg ttt ttc ttt gaa acc aca gct tat Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Glu Thr Thr Ala Tyr	336
100 105 110	
caa tat ggc aat gct gcg aat gta gta gtt gta tta atg gca tcg gct Gln Tyr Gly Asn Ala Ala Asn Val Val Val Leu Met Ala Ser Ala	384
115 120 125	
gcc gta tct gcc ttg ata ttg gac agc ata ctg tta gat gaa cgt att Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile	432
130 135 140	
tgc att tct tca gtc gtc ggt gtg ggt ttg gca gta ttg ggg atc gca Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala	480
145 150 155 160	
atg att tct tgg act gga gaa gga agt tta ggg ttg att ctg aat gcc Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala	528
165 170 175	
gca ctg gcg ggc tcg ggc tac ggt tgt ttt tcc gtt ttg att aag aaa Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys	576
180 185 190	
ttc ggc cta aac ggc ggt att tat ttg aca cgg ata ttg atg ttt ttt Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe	624
195 200 205	
gga agt att ttt ttg ttt atc cct tca ttg gaa ggt att gag gat ata Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile	672
210 215 220	
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225 230 235 240	
ccg acg att tta gga ttt tat tgt aca act aaa gca ttg gat tat ttg Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu	768
245 250 255	
agt gct gcg aag gta cag gta act gaa ttg gcc gag cca ttg ttt gct Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala	816

260

265

270

gcc gta ctg gct tgg t~~t~~<sup>t</sup> ttt ttg aat gaa ata ccg gaa gga cgc ttc 864  
 Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe  
 275 280 285

ttt gtc ggc gcc att ctg att att gcc ggt att gtg tct atc aat ggg 912  
 Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly  
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Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val  
 35 40 45

Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser  
 50 55 60

Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser  
 65 70 75 80

Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Leu Lys Vál Ala Ile Cys  
 85 90 95

Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr  
 100 105 110

Gln Tyr Gly Asn Ala Ala Asn Val Val Val Val Leu Met Ala Ser Ala  
 115 120 125

Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile  
 130 135 140

Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala  
 145 150 155 160

Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala  
 165 170 175

Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys  
 180 185 190

Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe  
 195 200 205

Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile  
 210 215 220

His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu  
 225 230 235 240

Pro	Thr	Ile	Leu	Gly	Phe	Tyr	Cys	Thr	Thr	Lys	Ala	Leu	Asn	Tyr	Leu
					245					250				255	
Ser	Ala	Ala	Lys	Val	Gln	Val	Thr	Glu	Leu	Ala	Glu	Pro	Leu	Phe	Ala
					260			265				270			
Ala	Val	Leu	Ala	Trp	Leu	Phe	Leu	Asn	Glu	Ile	Pro	Glu	Gly	Arg	Phe
					275			280			285				
Phe	Val	Gly	Ala	Ile	Leu	Ile	Ile	Ala	Gly	Ile	Val	Ser	Ile	Asn	Gly
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1						5				10					15		
gaa	tac	tac	gac	gcg	cgt	gcg	gct	tgt	gag	gac	atc	aag	ccc	ggc	tct	96	
Glu	Tyr	Tyr	Asp	Ala	Arg	Ala	Ala	Cys	Glu	Asp	Ile	Lys	Pro	Gly	Ser		
20						25					30						
tac	gac	aag	ctg	cct	tac	acg	agc	cgc	att	ttg	gct	gag	aat	ttg	gtc	144	
Tyr	Asp	Lys	Leu	Pro	Tyr	Thr	Ser	Arg	Ile	Leu	Ala	Glu	Asn	Leu	Val		
35						40					45						
aac	cgc	gct	gac	aaa	gtc	gat	ttg	ccg	acg	ctg	caa	agc	tgg	ctg	ggt	192	
Asn	Arg	Ala	Asp	Lys	Val	Asp	Leu	Pro	Thr	Leu	Gln	Ser	Trp	Leu	Gly		
50						55					60						
cag	ctg	att	gag	gga	aaa	cag	gaa	atc	gac	ttt	cct	tgg	tat	ccg	gct	240	
Gln	Leu	Ile	Glu	Gly	Lys	Gln	Glu	Ile	Asp	Phe	Pro	Trp	Tyr	Pro	Ala		
65						70				75					80		
cg	gt	gt	tgc	cac	gat	att	ctg	gg	cag	acc	g	tt	gt	gt	gat	tt	288
Arg	Val	Val	Cys	His	Asp	Ile	Leu	Gly	Gln	Thr	Ala	Leu	Val	Asp	Leu		
85						90					95						
gca	ggt	ctg	cgc	gat	g	cc	g	aa	aaa	gg	gg	gat	cct	gg	aaa	336	
Ala	Gly	Leu	Arg	Asp	Ala	Ile	Ala	Glu	Lys	Gly	Gly	Asp	Pro	Ala	Lys		
100						105					110						
gt	at	cc	gt	gt	g	aa	aaa	cc	ag	tc	at	gt	ac	ca	tc	384	
Val	Asn	Pro	Val	Val	Ala	Lys	Pro	Ser	Phe	Ile	Val	Asp	His	Ser	Leu		
115						120					125						
gg	tt	gaa	tgc	gg	tg	cc	g	cc	g	at	gg	tt	cg	aaa	ac	432	
Ala	Val	Glu	Cys	Gly	Tyr	Asp	Pro	Asp	Ala	Phe	Arg	Lys	Asn	Arg			
130						135					140						
caa	atc	gaa	gac	aga	cgt	aa	cc	gac	cc	gat	gg	tt	cg	aaa	ac	480	
Gln	Ile	Glu	Asp	Arg	Arg	Asn	Glu	Asp	Arg	Phe	His	Phe	Ile	Asn	Trp		
145						150					155				160		

卷之三

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Thr Lys Thr Ala Phe Gln Asn Val Asp Val Ile Pro Ala Gly Asn Gly			
165	170	175	
atc atg cac caa atc aat cta gaa aaa atg tcg ccc gtc gtc caa gtc			576
Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val			
180	185	190	
aaa aac ggc gtg gcg ttc ccc gat acc tgc gtc ggc acg gat tcg cac			624
Lys Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His			
195	200	205	
acg ccg cac gtc gat gct ctg ggc gtg att tcc gtg ggc gtg ggc gga			672
Thr Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly			
210	215	220	
ttg gaa gcg gaa acc gtg atg ctg ggt cgc gcg tcc atg atg cgc ctg			720
Leu Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu			
225	230	235	240
ccc gat att gtc ggc gtt gag ctg aac ggc aaa cgg cag gcg ggc att			768
Pro Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Gln Ala Gly Ile			
245	250	255	
acg gcg acg gat att gtg ttg gca ctg acc gag ttt ctg cgc aaa gaa			816
Thr Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu			
260	265	270	
cgc gtg gtc ggg gcg ttt gtc gaa ttc ttc ggc gag ggc gcg aga agc			864
Arg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser			
275	280	285	
ctg tct atc ggc gac cgc gcg acc att tcc aac atg acg ccg gag ttc			912
Leu Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe			
290	295	300	
ggc gcg act gcc gcg atg ttc gct att gat gag caa acc att gat tat			960
Gly Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr			
305	310	315	320
ttg aaa ctg acc gga cgc gac gac gcg cag gtg aaa ttg gtg gaa acc			1008
Leu Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr			
325	330	335	
tac gcc aaa acc gca ggc tta tgg gca gat gcc ttg aaa acc gcc gtt			1056
Tyr Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val			
340	345	350	
tat ccg cgc gtt ttg aaa ttt gat ttg agc agc gta acg cgc aat atg			1104
Tyr Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met			
355	360	365	
gca ggc ccg agc aac ccg cac gcg cgt ttt gcg acc gcc gat ttg gcc			1152
Ala Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala			
370	375	380	
agc aaa ggc ttg gct aaa cct tac gaa gag cct tca gac ggc caa atg			1200
Ser Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met			
385	390	395	400
ccc gac ggc gcg gtc atc atc gcc gcg att acc agt tgc acc aac act			1248
Pro Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr			
405	410	415	
tcc aac ccg cgc aac gtt gtt gcc gcc gcg ctc ttg gcg cgc aac gcc			1296

Ser Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala  
420. 425 426

aac tgc ttc ggg ctg aaa cgc aaa ccg tgg gtc aaa acc tcg ttt gcc 1344  
Asn Cys Phe Gly Leu Lys Arg Lys Pro Trp Val Lys Thr Ser Phe Ala  
435 440 445

ccc ggt tcg aaa gtg gcg gaa att tat ttg aaa gaa gca ggc ctg ctg 1392  
Pro Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Gly Leu Leu  
450 455 460

ccc gaa atg gaa aaa ctc ggc ttc ggt atc gtc gcc ttc gcc tgc acc 1440  
Pro Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr  
465 470 475 480

acc tgc aac ggc atg agt ggc gcg ctg gat ccg aaa atc cag aaa gaa 1488  
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485 490 495

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Ile Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg  
500 505 510

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Asn Phe Asp Gly Arg Val His Pro Tyr Ala Lys Gln Ala Phe Leu Ala  
515 520 525

tcg cct ccg ttg gtc gtt gcc tac gcg ctg gca ggc agt atc cgt ttc 1632  
Ser Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe  
530 535 540

gat att gaa aac gac gta ctc ggc gtt gca gac ggc aag gaa atc cgc 1680  
Asp Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg  
545 550 555 560

ctg aaa gac att tgg cct gcc gat gaa gaa atc gat gcc gtc gtt gcc 1728  
Leu Lys Asp Ile Trp Pro Ala Asp Glu Glu Ile Asp Ala Val Val Ala  
565 570 575

gaa tat gtg aaa ccg cag cag ttc cgc gat gtg tat gta ccg atg ttc 1776  
Glu Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Val Pro Met Phe  
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gac acc ggc aca gcg caa aaa gca cct agt ccg ctg tac gat tgg cgt 1824  
Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg  
595 600 605

ccg atg tcc acc tac atc cgc cgt ccg cct tac tgg gaa ggc gcg ctg 1872  
Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu  
610 615 620

gca ggg gaa cgc aca tta aga ggt atg cgt ccg ctg gcg att ttg ccc 1920  
Ala Gly Glu Arg Thr Leu Arg Gly Met Arg Pro Leu Ala Ile Leu Pro  
625 630 635 640

gac aac atc acc acc gac cac ctc tcg ccg tcc aat gcg att ttg gcc 1968  
Asp Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala  
645 650 655

gtc agt gcc gca ggc gag tat ttg gcg aaa atg ggt ttg cct gaa gaa 2016  
Val Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu  
660 665 670

gac ttc aac tct tac gca acc cac cgc ggc gac cac ttg acc gcc caa 2064  
Asp Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln  
675 680 685

cgc gct acc ttc.gcc	ccg aaa ctg ttt aac gaa atg gaa aa aac Arg Ala Thr Phe Ala ASN Pro Lys Leu Phe Asn Glu Met Val Lys Asn 690 695 700	2112
gaa gac ggc agc gtg cgc caa ggc tcg ttc gcc cgc gtc gaa ccc gaa Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu 705 710 715 720	2160	
ggc gaa acc atg cgc atg tgg gaa gcc atc gaa acc tat atg aac cgc Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg 725 730 735	2208	
aaa cag ccg ctc atc atc att gcc ggt gcg gac tat ggt caa ggc tca Lys Gln Pro Leu Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser 740 745 750	2256	
agc cgc gac tgg gct gca aaa ggc gta cgc ctc gcc ggc gta gaa gcg Ser Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala 755 760 765	2304	
att gtt gcc gaa ggc ttc gag cgt atc cac cgc acc aac ctt atc ggc Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly 770 775 780	2352	
atg ggc gtg ttg ccg ctg cag ttc aaa ccc gac acc aac cgc cat acc Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr 785 790 795 800	2400	
ctg caa ctg gac ggt acg gaa acc tac gac gtg gtc ggc gaa cgc aca Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr 805 810 815	2448	
ccg cgc tgc gac ctg acc ctc gtg att cac cgt aaa aac ggc gaa acc Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr 820 825 830	2496	
gtc gaa gtt ccc gtt acc tgc cgc ctc gat act gca gaa gaa gta ttg Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu 835 840 845	2544	
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Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val 35 40 45		
Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly		

50

55

60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala  
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Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu  
85 90 95

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys  
100 105 110

Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp His Ser Leu  
115 120 125

Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg  
130 135 140

Gln Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp  
145 150 155 160

Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly  
165 170 175

Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val  
180 185 190

Lys Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His  
195 200 205

Thr Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly  
210 215 220

Leu Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu  
225 230 235 240

Pro Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Gln Ala Gly Ile  
245 250 255

Thr Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu  
260 265 270

Arg Val Val Gly Ala Phe Val Glu Phe Gly Glu Gly Ala Arg Ser  
275 280 285

Leu Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe  
290 295 300

Gly Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr  
305 310 315 320

Leu Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr  
325 330 335

Tyr Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val  
340 345 350

Tyr Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met  
355 360 365

Ala Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala  
370 375 380

Ser Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met  
385 390 395 400

Pro Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr

405

410

415

Ser Asn Pro Arg Asn Val Ala Ala Ala Leu Leu Ala Arg Asn Ala  
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Pro Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Gly Leu Leu  
 450 455 460

Pro Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr  
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Thr Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu  
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Ile Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg  
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Asn Phe Asp Gly Arg Val His Pro Tyr Ala Lys Gln Ala Phe Leu Ala  
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Ser Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe  
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Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg  
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Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu  
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Ala Gly Glu Arg Thr Leu Arg Gly Met Arg Pro Leu Ala Ile Leu Pro  
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Val Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu  
 660 665 670

Asp Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln  
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Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn  
 690 695 700

Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu  
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Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg  
 725 730 735

Lys Gln Pro Leu Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser  
 740 745 750

Ser Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala

755

760

765

Ile Val Ala Glu Gly Ile Glu Arg Ile His Arg Thr Asn Leu Ile Gly  
770 775 780

Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr  
785 790 795 8000

Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr  
805 810 815

Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr  
 820 825 830

Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu  
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gcg gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc ccg 144  
 Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro  
           35                40                45

gac ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agt tcg tcc 192  
 Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser  
       50                 55                 60

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Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp
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Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
          85           90           95

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Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala  
100 105 110

atc gag caa ggc ttg gtc gat aaa tcc aaa atc cct tca gac ggc ccg 384  
Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro  
115 120 125

tgt acc gtc aaa atc	cag aaa aac atc ggc aaa acc a	ttt gcc	432
Cys Thr Val Lys Ile	Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala		
130	135	140	
cat gta ccg atg caa aac ggc gca gtt ttg gaa aca ggc gat ttt gag			480
His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu			
145	150	155	160
ctc gac ggc gta acg ttc ccg gca gcc gaa gta' caa atc gaa ttt ctt			528
Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu			
165	170	175	
gat cca gcc gac ggc gaa ggc agt atg ttc cca acc ggc aat ttg gtc			576
Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val			
180	185	190	
gat gaa att gat gtg ccg aat ata ggc cgt ttg aaa gcc acg ctc atc			624
Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile			
195	200	205	
aac gcg ggc att ccg acc gtt ttc ctg aat gcc gac ttg ggc tac			672
Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr			
210	215	220	
acg ggc aaa gag ttg caa gac gac atc aac aac gat gcc gca gct ttg			720
Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu			
225	230	235	240
gaa aaa ttc gag aaa atc cgc gct tac ggt gcg ctg aaa atg ggt cta			768
Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu			
245	250	255	
atc agc gac gta tcc gaa gct gcc gcc cgcc cac acg ccg aaa gtc			816
Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val			
260	265	270	
gcc ttc gtc gcg ccc gcc gat tac acc gcc tcc agt ggc aaa acc			864
Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr			
275	280	285	
gtg aat gcc gcc gac atc gat ttg ctg gta cgc gcc ctg agc atg ggc			912
Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly			
290	295	300	
aaa ttg cac cac gcg atg atg ggt acc gcc tct gtt gcc att gcg acc			960
Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr			
305	310	315	320
gcc gcc gcc gtg ccc ggt acg ctg gtc aac ctt gcc gca ggg gcg gga			1008
Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly			
325	330	335	
acg cgt aaa gaa gtg cgc ttc ggg cat cct tcc ggc aca ttg cgc gtc			1056
Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val			
340	345	350	
ggt gca gcc gcc gaa tgt cag gac gga caa tgg acg gcc acc aaa gcg			1104
Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala			
355	360	365	
gtt atg agc cgc agc gca cgc gtg atg gaa ggt tgg gtc agg gtg			1152
Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val			
370	375	380	
ccg gaa gat tgt ttt taa			1170

Pro Glu Asp Cys Phe  
385

<210> 44  
<211> 389  
<212> PRT  
<213> Neisseria meningitidis

<400> 44  
Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser  
1 5 10 15  
  
Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu  
20 25 30  
  
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro  
35 40 45  
  
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser  
50 55 60  
  
Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp  
65 70 75 80  
  
Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp  
85 90 95  
  
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala  
100 105 110  
  
Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro  
115 120 125  
  
Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala  
130 135 140  
  
His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu  
145 150 155 160  
  
Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu  
165 170 175  
  
Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val  
180 185 190  
  
Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile  
195 200 205  
  
Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr  
210 215 220  
  
Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu  
225 230 235 240  
  
Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu  
245 250 255  
  
Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val  
260 265 270  
  
Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr  
275 280 285  
  
Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly  
290 295 300

Lys Leu His His Ala Met Gly Thr Ala Ser Val Ala Ile Thr  
305 310 315 320

Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly  
325 330 335

Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val  
340 345 350

Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala  
355 360 365

Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val  
370 375 380

Pro Glu Asp Cys Phe  
385

<210> 45

<211> 954

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)...(951)

<400> 45

atg cgc acg ccg ttt tgt tgg gca tac gcc aat gcc gcc cga ata tcg 48  
Met Arg Thr Pro Phe Cys Trp Ala Tyr Ala Asn Ala Ala Arg Ile Ser  
1 5 10 15

gca atg ctg ccg gcg tgt tgg gcg cag gcg atg ttg gcc gaa gta atc 96  
Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile  
20 25 30

agc tgc aac aag gct tcg ctg ccg cag cct tcg gcg aga tcg gcg 144  
Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala  
35 40 45

ttt aaa tca acc tgc ttc atg ggt gat tct ccg tat ttg gtt cag ata 192  
Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile  
50 55 60

gac ttg gtt ttt gcg ccg cag ggc ggt ggc ttc ttt caa gcc gat tat 240  
Asp Leu Val Phe Ala Pro Gln Gly Gly Phe Phe Gln Ala Asp Tyr  
65 70 75 80

ttt gaa ttt gac ttt gct gcc gaa gcg cac ctg tgc cag cct gcc caa 288  
Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln  
85 90 95

atc ggc ggc aac ggt agc gat ttt cgg ata acc gcc ggt ggt ttg 336  
Ile Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu  
100 105 110

cgc atc ggc cag cag gat aat cgg ttt gcc gcc ggg cgg cac ctg cac 384  
Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His  
115 120 125

ggt tcc tgc ctg aac agc gtg gga cag cat ttc caa agg ttg cga cag 432  
Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln  
130 135 140

ggt cag cgg ctg tcc gaa gcg gta gcc cat gcg gtt gtc gct 480  
 Gly Gln Arg Leu Ser Glu Ala Val Ala His Ala Val Ala Ile Ala  
 145 150 155 160

ttg cag cgt cca cgt ttc ccg ttc cag att cag acg ccc ttt ttc act 528  
 Leu Gln Arg Pro Arg Phe Pro Phe Gln Ile Gln Thr Pro Phe Phe Thr  
 165 170 175

gaa agc ggc ata ttc cga cga agg aac aag gtg gat ggt atc ggt aaa 576  
 Glu Ser Gly Ile Phe Arg Arg Asn Lys Val Asp Gly Ile Gly Lys  
 180 185 190

cggtatccggggcaatgccgactttggacaatccctgcgcacccttggcc 624  
 Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Thr Phe Ala  
 195 200 205

gat ggg gag ata atc gcc ttt ttg cag cat tct gcc ctg atg gcc gcc 672  
 Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala  
 210 215 220

gaa acc ggc ttt cag gtc ggt gct tct cga acc cat cac ttc cgg cac 720  
 Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His  
 225 230 235 240

atc aaa tcc gcc cgc cac gca cac ata gcc gta cat gcc ctg cac ggc 768  
 Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly  
 245 250 255

acg cac cat ttt caa ggt ctg ccc ttt gcg ggc ggt ata acg cca ata 816  
 Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile  
 260 265 270

cga ata gac cgg ttc gcc gtc caa ttc cgc ctg ata cac ggc acc ggt 864  
 Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly  
 275 280 285

gag aca aaa cgg cgt atc ccg ttc aaa cac cag cat tat ccc gcc caa 912  
 Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln  
 290 295 300

agc gat ttc gat tgc ggc cgt gcc ttc gtc gtt gcc caa taa 954  
 Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln  
 305 310 315

<210> 46

<211> 317

<212> PRT

<213> Neisseria meningitidis

<400> 46

Met Arg Thr Pro Phe Cys Trp Ala Tyr Ala Asn Ala Ala Arg Ile Ser  
 1 5 10 15

Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile  
 20 25 30

Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala  
 35 40 45

Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile  
 50 55 60

Asp Leu Val Phe Ala Pro Gln Gly Gly Phe Phe Gln Ala Asp Tyr  
 65 70 75 80

Phe Glu Phe Asp .Phe Ala Glu Ala His Leu Cys Gln Pala Gln  
 85 90 95

Ile Gly Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu  
 100 105 110

Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His  
 115 120 125

Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln  
 130 135 140

Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala  
 145 150 155 160

Leu Gln Arg Pro Arg Phe Pro Phe Gln Ile Gln Thr Pro Phe Phe Thr  
 165 170 175

Glu Ser Gly Ile Phe Arg Arg Arg Asn Lys Val Asp Gly Ile Gly Lys  
 180 185 190

Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Thr Phe Ala  
 195 200 205

Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala  
 210 215 220

Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His  
 225 230 235 240

Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly  
 245 250 255

Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile  
 260 265 270

Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly  
 275 280 285

Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln  
 290 295 300

Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln  
 305 310 315

<210> 47  
 <211> 648  
 <212> DNA  
 <213> Neisseria meningitidis

<220>  
 <221> CDS  
 <222> (1)..(645)

<400> 47  
 atg aga ata gag atc aca cca atc agc gaa tcc gct ttg gtc tgc cga 48  
 Met Arg Ile Glu Ile Thr Pro Ile Ser Glu Ser Ala Leu Val Cys Arg  
 1 5 10 15

ctg aat gcg cct tcc gaa ctg ggc aaa cag caa aag ttg tgg gcg ttt 96  
 Leu Asn Ala Pro Ser Glu Leu Gly Lys Gln Gln Lys Leu Trp Ala Phe  
 20 25 30

TOP 1000 E. coli genes

gcc gct gcg ctc ggg cag cac gac agg att gag gaa gtg gta gtc ggc Ala Ala Ala Leu .Gly His Asp Arg Ile Glu Glu Val Val Gly 35 40 45	144	
atg aac aat ctg acc gtg ttc acc cgt ttc gat acc gat ttg gcg acg Met Asn Asn Leu Thr Val Phe Thr Arg Phe Asp Thr Asp Leu Ala Thr 50 55 60	192	
ctt gcc gat gaa ttg caa tat gtg tgg gaa cac acc gcc gtt aca gac Leu Ala Asp Glu Leu Gln Tyr Val Trp Glu His Thr Ala Val Thr Asp 65 70 75 80	240	
cat cag ggc aaa ctg gtg gaa att ccc gtc tgc tac ggc ggc gaa tac His Gln Gly Lys Leu Val Glu Ile Pro Val Cys Tyr Gly Gly Glu Tyr 85 90 95	288	
ggc ccg gat ttg gcg gaa gtc gct gtc cat cag acg gtt att tcc Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser 100 105 110	336	
gaa atc gtc cgc cgc cat acg gcg caa act tat acc gta ttt atg atg Glu Ile Val Arg Arg His Thr Ala Gln Thr Tyr Thr Val Phe Met Met 115 120 125	384	
ggc ttc cag cct ggt ttc cct tat ctg ggc ggc ttg ccc gaa gca ttg Gly Phe Gln Pro Gly Phe Pro Tyr Leu Gly Gly Leu Pro Glu Ala Leu 130 135 140	432	
cac acg ccc cgc cgt gcc gtg ccg aga acg tcc gtt cct gcc ggt tcg His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser 145 150 155 160	480	
gtc ggt atc ggc ggc agt cag acc ggt gtg tat ccg ttc gct tcg ccc Val Gly Ile Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro 165 170 175	528	
ggc ggc tgg cag att atc ggc aga acc gaa tta ccc ttg ttc cga gcc Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala 180 185 190	576	
gat ttg aat ccg ccg acc ctg ctg gcg ggc ggt gac caa gtc cgc ttt Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe 195 200 205	624	
gtt gca gaa agg att gag cca tga Val Ala Glu Arg Ile Glu Pro 210 215	648	
<210> 48		
<211> 215		
<212> PRT		
<213> Neisseria meningitidis		
<400> 48		
Met Arg Ile Glu Ile Thr Pro Ile Ser Glu Ser Ala Leu Val Cys Arg 1 5 10 15		
Leu Asn Ala Pro Ser Glu Leu Gly Lys Gln Gln Lys Leu Trp Ala Phe 20 25 30		
Ala Ala Ala Leu Gly Gln His Asp Arg Ile Glu Glu Val Val Val Gly 35 40 45		
Met Asn Asn Leu Thr Val Phe Thr Arg Phe Asp Thr Asp Leu Ala Thr 50 55 60		

Leu Ala Asp Glu Leu Cys Tyr Val Trp Glu His Thr Ala Val Ser Asp  
65 75 80

His Gln Gly Lys Leu Val Glu Ile Pro Val Cys Tyr Gly Gly Glu Tyr  
85 90 95

Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser  
100 105 110

Glu Ile Val Arg Arg His Thr Ala Gln Thr Tyr Thr Val Phe Met Met  
115 120 125

Gly Phe Gln Pro Gly Phe Pro Tyr Leu Gly Gly Leu Pro Glu Ala Leu  
130 135 140

His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser  
145 150 155 160

Val Gly Ile Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro  
165 170 175

Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala  
180 185 190

Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe  
195 200 205

Val Ala Glu Arg Ile Glu Pro  
210 215

<210> 49

<211> 930

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(927)

<400> 49

atg att cac gtt tcg gca gtg cag gca ccg gcg cat att cag gat acc  
Met Ile His Val Ser Ala Val Gln Ala Pro Ala His Ile Gln Asp Thr  
1 5 10 15

gga cgc tac gga cac cgg cgt tac ggc atc ggt cat gcc ggt gcg atg  
Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met  
20 25 30

gac acg gtt gct ttg gcg ggt aat att tta ttg ggc aac gac gaa  
Asp Thr Val Ala Ala Gly Asn Ile Leu Gly Asn Asp Glu  
35 40 45

ggc acg gcc gca atc gaa atc gct ttg ggc ggg ata atg ctg gtg ttt  
Gly Thr Ala Ala Ile Glu Ala Leu Gly Gly Ile Met Leu Val Phe  
50 55 60

gaa cgg gat acg ccg ttt tgt ctc acc ggt gcc gtg tat cag gcg gaa  
Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu  
65 70 75 80

ttg gac ggc gaa ccg gtc tat tcg tat tgg cgt tat acc gcc cgc aaa  
Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys  
85 90 95

ggg cag acc ttg aaa ggtgt cgt gcc gtg cag ggc atg ta c tat 336  
Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Tyr  
100 105 110

gtg tgc gtg gcg ggc gga ttt gat gtg ccg gaa gtg atg ggt tcg aga 384  
Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg  
115 120 125

agc acc gac ctg aaa gcc ggt ttc ggc ggc cat cag ggc aga atg ctg 432  
Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu  
130 135 140

caa aaa ggc gat tat ctc ccc atc ggc aaa ggt gcg cag gaa ttg tcc 480  
Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser  
145 150 155 160

aaa gtc ggc att gcc ccg ata ccg ttt acc gat acc atc cac ctt gtt 528  
Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val  
165 170 175

cct tcg tcg gaa tat gcc gct ttc agt gaa aaa ggg cgt ctg aat ctg 576  
Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu  
180 185 190

gaa cgg gaa acg tgg acg ctg caa agc gat agc aac cgc atg ggc tac 624  
Glu Arg Glu Thr Trp Thr Leu Gln Ser Asp Ser Asn Arg Met Gly Tyr  
195 200 205

cgc ttc gac gga cag ccg ctg acc ctg tcg caa cct ttg gaa atg ctg 672  
Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu  
210 215 220

tcc cac gct gtt cag gca gga acc gtg cag gtg ccg ccc ggc ggc aaa 720  
Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys  
225 230 235 240

ccg att atc ctg ctg gcc gat gcg caa acc acc ggc ggt tat ccg aaa 768  
\*Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys  
245 250 255

atc gct acc gtt gcc gcc gat ttg ggc agg ctg gca cag gtg cgc 816  
Ile Ala Thr Val Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg  
260 265 270

ttc ggc agc aaa gtc aaa ttc aaa ata atc ggc ttg aaa gaa gcc acc 864  
Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr  
275 280 285

gcc ctg cgg cgc aaa aac caa gtc tat ctg aac caa ata cgg aga atc 912  
Ala Leu Arg Arg Lys Asn Gln Val Tyr Leu Asn Gln Ile Arg Arg Ile  
290 295 300

acc cat gaa gca ggt tga 930  
Thr His Glu Ala Gly  
305

<210> 50

<211> 309

<212> PRT

<213> Neisseria meningitidis

<400> 50

Met Ile His Val Ser Ala Val Gln Ala Pro Ala His Ile Gln Asp Thr  
1 5 10 15

Gly Arg Tyr Gly His . . . Arg Tyr Gly Ile Gly His Ala G . . . Ala Met  
20 25 30

Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu  
35 40 45

Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe  
50 55 60

Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu  
65 70 75 80

Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys  
85 90 95

Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr  
100 105 110

Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg  
115 120 125

Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu  
130 135 140

Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser  
145 150 155 160

Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val  
165 170 175

Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu  
180 185 190

Glu Arg Glu Thr Trp Thr Leu Gln Ser Asp Ser Asn Arg Met Gly Tyr  
195 200 205

Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu  
210 215 220

Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys  
225 230 235 240

Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys  
245 250 255

Ile Ala Thr Val Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg  
260 265 270

Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr  
275 280 285

Ala Leu Arg Arg Lys Asn Gln Val Tyr Leu Asn Gln Ile Arg Arg Ile  
290 295 300

Thr His Glu Ala Gly  
305

<210> 51  
<211> 2094  
<212> DNA  
<213> Neisseria meningitidis

<220>

<221> CDS  
<222> (1)...(2091)

<400> 51  
atg aat tcg acc gca agt aaa acc ctg aaa gga ttg tcg ctg gtg ttt 48  
Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe  
1 5 10 15

ttc gcc tct gga ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96  
Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg  
20 25 30

ctt cta ttc agt cac ata ggt atc gat ttg agt tcg att act gtc att 144  
Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile  
35 40 45

att tct gta ttt atg gtc ggc ttg ggt gta ggt gcg tat ttc ggt gga 192  
Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly  
50 55 60

cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc 240  
Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile  
65 70 75 80

gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc agg ggt ctg att 288  
Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Arg Gly Leu Ile  
85 90 95

tcc ggc ttg ggg cat ctt tta gtt gag gct gat ttg ccc atc atc gct 336  
Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala  
100 105 110

gct gcc aat ttc ctc tta ttg ctg ctt cct acc ttt atg atg ggc gcg 384  
Ala Ala Asn Phe Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala  
115 120 125

acc ttg ccc ttg ctg acc tgt ttt aac cgg aaa ata cat aat gtt 432  
Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val  
130 135 140

ggc gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt gcg gca 480  
Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala  
145 150 155 160

ctc gga tcg ctt gcc gcc gaa ttt ttc tac gtc ttt ttt acc ctc 528  
Leu Gly Ser Leu Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu  
165 170 175

tcc caa acc att gcg ctg aca gcc tgc ttt aac ctt ctg att gct gct 576  
Ser Gln Thr Ile Ala Leu Thr Ala Cys Phe Asn Leu Leu Ile Ala Ala  
180 185 190

tca gta tgc tgc gtt aca gaa agg atg gat ata gtg aac act aaa ccg 624  
Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro  
195 200 205

aat act agt ttg att tat atg ctt tct ttc ctt agc ggc tta ttg agc 672  
Asn Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser  
210 215 220

ttg ggt ata gaa gtc ttg tgg gta agg atg ttt tcg ttc gca gca cag 720  
Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln  
225 230 235 240

tcc gtg cct cag gca ttt tca ttt act ctt gcc tat ttt ctg acc ggt 768  
Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly

245

250

255

atc gcc gtc ggc gcg	ttt ggc aaa cgg att tgc cgc agc ggc ttt	816	
Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe			
260	265	270	
gtt gat att ccc ttt atc ggg cag tgc ttc ttg tgg gcg ggt att gcc	864		
Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala			
275	280	285	
gac ttt ttg att ttg ggt gct gcg tgg ttg acg ggt ttt tcc ggc	912		
Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly			
290	295	300	
ttc gtc cac cac gcc ggt atc ttc att acc ctg tct gcc gtc gtc aga	960		
Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg			
305	310	315	320
ggg ttg att ttc ccg ctc gta cac cat gtg ggt acg gat ggc aac aaa	1008		
Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys			
325	330	335	
tcc gga cga cag gtt tcc aat gtt tat ttc gcc aac gtt gcc ggc agt	1056		
Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser			
340	345	350	
gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttc ttg tcc	1104		
Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser			
355	360	365	
acc caa cag att tac ctg ctc atc tgt ttg att tct gct gct gtc cct	1152		
Thr Gln Gln Ile Tyr Leu Ile Cys Leu Ile Ser Ala Ala Val Pro			
370	375	380	
ttg ttt tgt aca ctg ttccaa aaa agt ctc cga ctg aat gca gtg tcg	1200		
Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser			
385	390	395	400
gta gca gtt tcc cta atg ttc ggc atc ctc atg ttc cta ctg ccg gat	1248		
Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp			
405	410	415	
tct gtc ttt caa aat att gct gac cgt ccg gat cgg ctg att gaa aac	1296		
Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn			
420	425	430	
aaa cac ggc att gtt gcg gtt tac cat aga gat ggt gat aag gtt gtt	1344		
Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val			
435	440	445	
tat ggg gcg aat gta tac gac ggc gca tac aat acc gat gta ttc aat	1392		
Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn			
450	455	460	
agt gtc aac ggc atc gaa cgt gcc tat ctg cta ccc tcc ctg aag tct	1440		
Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser			
465	470	475	480
ggc ata cgc cgc att ttc gtc gtt gga ttg agt aca ggt tcg tgg gcg	1488		
Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala			
485	490	495	
cgc gtc ttg tct gcc att ccg gaa atg cag tcg atg atc gtt gcg gaa	1536		
Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu			
500	505	510	

atc aat ccg gca tac cgt agc ctt atc gcg gac gag ccg caa atc gcc Ile Asn Pro Ala Tyr Ser Leu Ile Ala Asp Glu Pro Glu Le Ala	515	520	525	1584
ccg ctt ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt agg Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg	530	535	540	1632
aaa tgg ctg cgt cgc cat cct gat gaa aaa ttc gac ctg att ttg atg Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met	545	550	555	1680
aat acg act tgg tac tgg cgt gcc tat tcc acc aac ctg ttg agt gcg Asn Thr Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala	565	570	575	1728
gaa ttt tta aaa cag gtgcaa agc cac ctt acc ccg gat ggt att gta Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val	580	585	590	1776
atg ttt aat acc acg cac agc ccg cat gct ttt gct acc gcc gta cac Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His	595	600	605	1824
agt att ccc tat gca tac cgc tat ggg cat atg gta gtc ggc tcg gca Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala	610	615	620	1872
acc ccg gta gtt ttc cct aat aaa gaa ctg ctc aag caa cgt ctc tcc Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser	625	630	635	1920
cgg ttg att tgg ccg gaa agc ggc agg cac gta ttt gac agc agc acc Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr	645	650	655	1968
gtg gat gct gca gca caa aag gtt gtc tct cgt atg ctg att cag atg Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Gln Met	660	665	670	2016
acg gaa cct tcg gct ggg gcg gaa gtc att acc gac gat aat atg att Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile	675	680	685	2064
gta gaa tac aaa tac ggc aga ggg att taa Val Glu Tyr Lys Tyr Gly Arg Gly Ile	690	695		2094

<210> 52  
<211> 697  
<212> PRT  
<213> Neisseria meningitidis

<400> 52				
Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe	1	5	10	15
Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg	20	25	30	
Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile	35	40	45	
Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly	50	55	60	

Arg Ile Ala Asp Arg Pro Ser Ser Ile Ile Pro Leu Phe Ile  
65 75 80

Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Arg Gly Leu Ile  
85 90 95

Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala  
100 105 110

Ala Ala Asn Phe Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala  
115 120 125

Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val  
130 135 140

Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala  
145 150 155 160

Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu  
165 170 175

Ser Gln Thr Ile Ala Leu Thr Ala Cys Phe Asn Leu Leu Ile Ala Ala  
180 185 190

Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro  
195 200 205

Asn Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser  
210 215 220

Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln  
225 230 235 240

Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly  
245 250 255

Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe  
260 265 270

Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala  
275 280 285

Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly  
290 295 300

Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg  
305 310 315 320

Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys  
325 330 335

Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser  
340 345 350

Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser  
355 360 365

Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro  
370 375 380

Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser  
385 390 395 400

Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp  
405 410 415

Ser Val Phe Gln Asn      Ala Asp Arg Pro Asp Arg Leu I      lu Asn  
420                          425                          430

Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val  
435                          440                          445

Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn  
450                          455                          460

Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser  
465                          470                          475                          480

Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala  
485                          490                          495

Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu  
500                          505                          510

Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala  
515                          520                          525

Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg  
530                          535                          540

Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met  
545                          550                          555                          560

Asn Thr Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala  
565                          570                          575

Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val  
580                          585                          590

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His  
595                          600                          605

Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala  
610                          615                          620

Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser  
625                          630                          635                          640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr  
645                          650                          655

Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Gln Met  
660                          665                          670

Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile  
675                          680                          685

Val Glu Tyr Lys Tyr Gly Arg Gly Ile  
690                          695

<210> 53

<211> 1040

<212> PRT

<213> Neisseria meningitidis

<400> 53

Cys Leu Gly Gly Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly  
1                          5                          10                          15

Gly Thr Gly Ile Gly Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala  
20 . . 25 30 . .  
Ala Val Ser Tyr Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser  
35 40 45  
Met Leu Cys Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala  
50 55 60  
Lys Ile Asn Ala Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn  
65 70 75 80  
Pro Asn Asp Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu  
85 90 95  
Ala Gly Tyr Thr Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly  
100 105 110  
Glu Ser Val Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu  
115 120 125  
His Gly Tyr Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys  
130 135 140  
Glu Ala Pro Glu Asp Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp  
145 150 155 160  
Asp Glu Ala Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His  
165 170 175  
Val Lys Glu Ile Gly His Ile Asp Val Val Ser His Ile Ile Gly Gly  
180 185 190  
Arg Ser Val Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr  
195 200 205  
Leu His Ile Met Asn Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser  
210 215 220  
Ala Ala Ile Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg  
225 230 235 240  
Ile Val Asn Asn Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp  
245 250 255  
His Phe Gln Ile Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu  
260 265 270  
Ala Tyr Ser Gly Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln  
275 280 285  
Gln Ser Asp Tyr Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met  
290 295 300  
Leu Phe Ile Phe Ser Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr  
305 310 315 320  
Leu Thr Leu Leu Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile  
325 330 335  
Thr Val Ala Gly Val Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn  
340 345 350  
His Cys Gly Ile Thr Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala  
355 360 365

D995E410E8360

Ser Val Arg Phe Thr Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser  
370 . . . 375 380 . . .

Phe Ser Ala Pro Ile Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys  
385 390 395 400

Tyr Pro Trp Met Ser Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr  
405 410 415

Ala Gln Asp Ile Gly Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly  
420 425 430

Leu Leu Asp Ala Gly Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe  
435 440 445

Gly Asp Phe Thr Ala Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser  
450 455 460

Phe Arg Asn Asp Ile Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly  
465 470 475 480

Ser Gln Leu Gln Leu His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile  
485 490 495

Ile Glu Gly Gly Ser Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met  
500 505 510

Arg Val Glu Thr Lys Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly  
515 520 525

Gly Ser Leu Asn Ser Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg  
530 535 540

Ser Gly Ala Asn Glu Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly  
545 550 555 560

Gly Glu Gly Thr Leu Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp  
565 570 575

Gly Thr Ala Met Thr Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys  
580 585 590

Gly Ala Gly Tyr Leu Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser  
595 600 605

Ala Ala Lys Ile Gly Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr  
610 615 620

Asp Gly Gly Leu Leu Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly  
625 630 635 640

Ser Glu Gly Asp Thr Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala  
645 650 655

Arg Thr Ala Ser Ala Ala Ala His Ser Ala Pro Ala Gly Leu Lys His  
660 665 670

Ala Val Glu Gln Gly Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu  
675 680 685

Asp Ala Ser Glu Ser Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala  
690 695 700

Ala Asp Arg Thr Asp Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe  
705 710 715 720

Protein sequence

Arg Ala Ala Ala Ala Val Gln His Ala Asn Ala Ala Asp Gly Val Arg  
725 730

Ile Phe Asn Ser Leu Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala  
740 745 750

His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu  
755 760 765

Asp His Asn Ala Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp  
770 775 780

Gly Gly Thr Trp Glu Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser  
785 790 795 800

Thr Gln Thr Val Gly Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala  
805 810 815

Ala Ala Thr Leu Gly Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala  
820 825 830

Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp  
835 840 845

Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr  
850 855 860

Lys Asn Ser Ile Ser Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly  
865 870 875 880

Ser Val Asn Gly Thr Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn  
885 890 895

Val Pro Phe Ala Ala Thr Gly Asp Leu Thr Val Glu Gly Leu Arg  
900 905 910

Tyr Asp Leu Leu Lys Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu  
915 920 925

Gly Trp Ser Gly Asn Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala  
930 935 940

Gly Leu Lys Leu Ser Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala  
945 950 955 960

Thr Ala Gly Val Glu Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr  
965 970 975

Gly Gly Phe Thr Gly Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg  
980 985 990

Asn Met Pro His Thr Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu  
995 1000 1005

Phe Gly Asn Gly Trp Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser  
1010 1015 1020

Lys Gln Tyr Gly Asn His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe  
1025 1030 1035 1040

<211> 858  
<212> DNA  
<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(855)

<400> 54

atg tct gaa gaa aaa ttg aaa atg agt ttc gag cca acc gta atc gaa 48  
Met Ser Glu Glu Lys Leu Lys Met Ser Phe Glu Pro Thr Val Ile Glu  
1 5 10 15

cat ttg ggt gta aag atg tat tcg cac act gtt cct gcg att gcc gag 96  
His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu  
20 25 30

ttg ata gcg aat gcc tac gat gca tgt gct acg gaa gtg gaa gtt agg 144  
Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg  
35 40 45

tta ttc gat aaa ccg gag cat aaa atc gtt att aaa gat aat ggc ata 192  
Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile  
50 55 60

gga atg agc ttc gat gaa atc aat gat ttt tat ttg aga atc ggt cgg 240  
Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg  
65 70 75 80

aac aga agg gaa gaa aaa caa gcc tcc ccg tgc gga aga att cca acg 288  
Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr  
85 90 95

ggt aaa aaa ggt ctt ggt aaa ttg gca tta ttc agg ctt ggc aac aaa 336  
Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys  
100 105 110

atc gaa atc tct act atc caa gga aac gaa cgg gtt act ttt act ttg 384  
Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu  
115 120 125

gat tat gca gag att aaa aaa agt gag cgt att tat caa ccg gag ttt 432  
Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe  
130 135 140

cag aaa gag tct gtt aaa ccc aat acc gaa aac gga aca act ata act 480  
Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr  
145 150 155 160

tta acc gag ctg acg aaa aaa caa gga tac ccg tta gat aat tat gtg 528  
Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val  
165 170 175

ggg cat ctt tcc cgt tta ttt gat ttt ccg gct cag gat ttt aaa atc 576  
Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile  
180 185 190

aaa gta agc ttg aac ggc tcg gaa cca aga atc att gac gga aac cta 624  
Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu  
195 200 205

aaa tat aat ctt gtt acc cca caa ttc gaa tgg gaa tac cag gat cta 672  
Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu  
210 215 220

gca acc aat att tca tcg tta tct tca aaa ttc gaa cag tat gaa tac 720

Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr  
225 . 230 235 240

agc gga tta ata caa ggt aag ttc att aca acg gaa aaa cct tta aag 768  
Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys  
245 250 255

aat aat atg aaa ggt att acc ttg ttt gcc aac ggc aga atg gta aat 816  
Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn  
260 265 270

atg ccc gag ttt ttc act gat agc gaa tcc agc cat ttc taa 858  
Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe  
275 280 285

<210> 55  
<211> 285  
<212> PRT  
<213> Neisseria gonorrhoeae

<400> 55  
Met Ser Glu Glu Lys Leu Lys Met Ser Phe Glu Pro Thr Val Ile Glu  
1 5 10 15

His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu  
20 25 30

Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg  
35 40 45

Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile  
50 55 60

Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg  
65 70 75 80

Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr  
85 90 95

Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys  
100 105 110

Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu  
115 120 125

Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe  
130 135 140

Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr  
145 150 155 160

Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val  
165 170 175

Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile  
180 185 190

Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu  
195 200 205

Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu  
210 215 220

Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr  
225 . 230 235 240

Ser Gly Leu Ile Gln Gly s Phe Ile Thr Thr Glu Lys Pro Ile Lys  
245 250

Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn  
260 265 270

Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe  
275 280 285

<210> 56

<211> 1575

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(1572)

<400> 56

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Met Lys Lys Ser Leu Phe Val Leu Phe Leu Tyr Ser Ser Leu Leu Thr  
1 5 10 15

gcc agc gaa atc gcc tat cgc ttt gta ttc gga att gaa acc tta ccg 96  
Ala Ser Glu Ile Ala Tyr Arg Phe Val Phe Gly Ile Glu Thr Leu Pro  
20 25 30

gct gca aaa atg gcg gaa acg ttt gcg ctg aca ttt atg att gct gcg 144  
Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala  
35 40 45

ctg tat ctg ttt gcg cgt tat aag gct tcg cgg ctg ctg att gcg gtg 192  
Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val  
50 55 60

ttt ttc gcg ttc agc atg att gcc aac aat gtg cat tac gcg gtt tat 240  
Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr  
65 70 75 80

caa agc tgg atg acg ggt att aac tat tgg ctg atg ctg aaa gag gtt 288  
Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val  
85 90 95

acc gaa gtc ggc agc gcg ggc gcg tcg atg ttg gat aag ttg tgg ctg 336  
Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu  
100 105 110

cct gct ttg tgg ggc gtg gcg gaa gtc atg ttg ttt tgc agc ctt gcc 384  
Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala  
115 120 125

aag ttc cgc cgt aag acg cat ttt tct gcc gat ata ctg ttt gcc ttc 432  
Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe  
130 135 140

cta atg ctg atg att ttc gtg cgt tcg ttc gac acg aaa caa gag cac 480  
Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His  
145 150 155 160

ggg att tcg ccc aaa ccg aca tac agc cgc atc aaa gcc aat tat ttc 528  
Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe  
165 170 175

agc ttc ggt tat ttt gtc ggg cgc gtg ttg ccg tat cag ttg ttt gat Ser Phe Gly Tyr Phe Val Arg Val Leu Pro Tyr Gln Leu Phe Asp	180                    185                    190	576
tta agc aag atc cct gtg ttc aaa cag cct gct cca agc aaa atc ggg Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly	195                    200                    205	624
caa ggc agt att caa aat atc gtc ctg att atg ggc gaa agc gaa agc Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser	210                    215                    220	672
gcg gcg cat ttg aaa ttg ttt ggt tac ggg cgc gaa act tcg ccg ttt Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe	225                    230                    235                    240	720
tta acc cgg ctg tcg caa gcc gat ttt aag ccg att gtg aaa caa agt Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser	245                    250                    255	768
tat tcc gca ggc ttt atg acg gca gta tcc ctg ccc agt ttc ttt aac Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn	260                    265                    270	816
gtc ata ccg cac gcc aac ggc ttg gaa caa atc agc ggc ggc gat acc Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr	275                    280                    285	864
aat atg ttc cgc ctc gcc aaa gag cag ggc tat gaa acg tat ttt tac Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr	290                    295                    300	912
agt gcc cag gct gaa aac caa atg gca att ttg aac tta atc ggt aag Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys	305                    310                    315                    320	960
aaa tgg ata gac cat ctg att cag ccg acg caa ctt ggc tac ggc aac Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn	325                    330                    335	1008
ggc gac aat atg ccc gat gag aag ctg ctg ccg ttg ttc gac aaa atc Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile	340                    345                    350	1056
aat ttg cag cag ggc agg cat ttt atc gtg ttg cac caa cgc ggt tcg Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser	355                    360                    365	1104
cac gcc cca tac ggc gca ttg ttg cag cct caa gat aaa gta ttc ggc His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly	370                    375                    380	1152
gaa gcc gat att gtg gat aag tac gac aac acc atc cac aaa acc gac Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp	385                    390                    395                    400	1200
caa atg att caa acc gta ttc gag cag ctg caa aag cag cct gac ggc Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly	405                    410                    415	1248
aac tgg ctg ttt gcc tat acc tcc gat cat ggc cag tat gtg cgc caa Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln	420                    425                    430	1296
gat atc tac aat caa ggc acg gtg cag ccc gac agc tat att gtg cct Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro		1344

435

440

445

ctg gtt ttg tac agc ccg at aag gcc gtg caa cag gct gcc a cag 1392  
 Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln  
 450 455 460

gct ttt gcg cct tgc gag att gcc ttc cat cag cag ctt tca acg ttc 1440  
 Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe  
 465 470 475 480

ctg att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa 1488  
 Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu  
 485 490 495

ggc tcg gta aca ggc aac ctg att acg ggc gat gca ggc agc ttg aac 1536  
 Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn  
 500 505 510

att cgcc aac ggc aag gcg gaa tat gtt tat ccg caa taa 1575  
 Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln  
 515 520

<210> 57  
<211> 524  
<212> PRT  
<213> Neisseria gonorrhoeae

<400> 57  
Met Lys Lys Ser Leu Phe Val Leu Phe Leu Tyr Ser Ser Leu Leu Thr  
 1 5 10 15

Ala Ser Glu Ile Ala Tyr Arg Phe Val Phe Gly Ile Glu Thr Leu Pro  
 20 25 30

Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala  
 35 40 45

Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val  
 50 55 60

Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr  
 65 70 75 80

Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val  
 85 90 95

Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu  
 100 105 110

Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala  
 115 120 125

Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe  
 130 135 140

Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His  
 145 150 155 160

Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe  
 165 170 175

Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp  
 180 185 190

Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly

195

200

205

Gln Gly Ser Ile Gln Asn Val Leu Ile Met Gly Glu Ser Ser  
 210 215 220

Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe  
 225 230 235 240

Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser  
 245 250 255

Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn  
 260 265 270

Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr  
 275 280 285

Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr  
 290 295 300

Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys  
 305 310 315 320

Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn  
 325 330 335

Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile  
 340 345 350

Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser  
 355 360 365

His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly  
 370 375 380

Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp  
 385 390 395 400

Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly  
 405 410 415

Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln  
 420 425 430

Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro  
 435 440 445

Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln  
 450 455 460

Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe  
 465 470 475 480

Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu  
 485 490 495

Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn  
 500 505 510

Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln  
 515 520

&lt;210&gt; 58

&lt;211&gt; 1314

<212> DNA  
<213> Neisseria gonorrhoeae  
<220>  
<221> CDS  
<222> (1)..(1311)

<400> 58  
atg ctg acg ttt atc gga ttg ctg att atc ggg gtc atc gta tgg ctg 48  
Met Leu Thr Phe Ile Gly Leu Leu Ile Ile Gly Val Ile Val Trp Leu  
1 5 10 15

ttg ctg acg gaa aaa gtg tcg ccc atc atc gca tta atc ttg gtg ccg 96  
Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro  
20 25 30

ctg att ggg gcg ttg ctg gcg ggg ttt gat gta tcc caa tta aaa gaa 144  
Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu  
35 40 45

ttt tat tcg ggc ggc acg aaa tcg gtg acg cag att gtg att atg ttt 192  
Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe  
50 55 60

atg ttt tcc att ttg ttt gga atc atg aac gat gtg ggg ctg ttc 240  
Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe  
65 70 75 80

cgt ccg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg 288  
Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val  
85 90 95

gca gtg agt gtg ggg acg gtc ttg gtg tcg gtg gca cag ttg gac 336  
Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp  
100 105 110

ggg gcg ggc gcg acg acg ttt tta tcg gtc gtc ccc gcc ctt ttg ccg 384  
Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro  
115 120 125

ctt tac aag cgt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg 432  
Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu  
130 135 140

act tcc agc gcg ggg cta atc aac ctt ttg ccg cgg ggc ggg ccg atc 480  
Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile  
145 150 155 160

ggg cgg gtt gca agc gtg ttg ggc gca gat gtg ggc gaa ttg tat aaa 528  
Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys  
165 170 175

cct ttg ttg acg gtg caa att atc ggt gtg gtg ttt atc ctt gtg ctg 576  
Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Val Leu  
180 185 190

tcc ctg ttt ttg ggt gtg cgt gaa aaa agg cgg att gtc cgg gag ttg 624  
Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu  
195 200 205

ggc gcg ttg ccc gcc gtg gcg gat ttg ata aag ccg cgg cct ttg tcg 672  
Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser  
210 215 220

gaa gaa gaa caa aaa ttg gcg cgt ccg aaa ctg ttt tgg tgg aat gtc 720  
Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val

225	230	235	240
ctg ctg ttt ttg gcg gca agc ctg ctt ttt tcg ggc atc	245	250	ccg 768
Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro			
	255		
ccg ggt tat gta ttt atg ctg gct gca acg gcg gcg ttg ctt ttg aat			816
Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn	260	265	
		270	
tac cgc agc ccg cag gaa cag atg gag cgg att tat gcc cac gcc ggc			864
Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly	275	280	
		285	
ggc gcg gtg atg atg gcg tcc att att ttg gcg gca ggt acg ttt ttg			912
Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu	290	295	
		300	
ggg att ttg aag ggc gcg ggg atg ttg gac gcg att tcc aaa gac ctt			960
Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu	305	310	
		315	
320			
gtg cat atc ctg ccg gac gcg ttg ctg cct tat ctg cat att gcc atc			1008
Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile	325	330	
		335	
ggt gtg ttg ggt att ccg ctt gag ttg gtt ttg agt acg gac gct tat			1056
Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr	340	345	
		350	
tat ttc gga ctg ttt ccg att gtg gaa cag att acc tcg cag gcg ggc			1104
Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly	355	360	
		365	
gtt gca ccc gaa gcg gca ggc tat gcg atg ttg atc ggc agt atc gtc			1152
Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val	370	375	
		380	
ggt act ttt gtt acg ccg ctt tcg ccg gct ttg tgg atg ggt ttg ggt			1200
Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly	385	390	
		395	
400			
ttg gcg aaa ttg tcg atg ggc aaa cac atc cgt tat tcg ttt ttc tgg			1248
Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp	405	410	
		415	
gcg tgg ggt ttg tcg ctg gcg ata ttg gtc agt tcg ata gcg gca gga			1296
Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly	420	425	
		430	
atc gtg cct ctg ccg taa			1314
Ile Val Pro Leu Pro			
	435		

<210> 59  
<211> 437  
<212> PRT  
<213> *Neisseria gonorrhoeae*

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<400> 59
Met Leu Thr Phe Ile Gly Leu Leu Ile Ile Gly Val Ile Val Trp Leu
      1           5           10          15

Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro
      20          25          30

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Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Glu  
35 40 45

Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe  
50 55 60

Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe  
65 70 75 80

Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val  
85 90 95

Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp  
100 105 110

Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro  
115 120 125

Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu  
130 135 140

Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile  
145 150 155 160

Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys  
165 170 175

Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Val Leu  
180 185 190

Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu  
195 200 205

Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser  
210 215 220

Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val  
225 230 235 240

Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro  
245 250 255

Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Asn  
260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly  
275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu  
290 295 300

Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu  
305 310 315 320

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile  
325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr  
340 345 350

Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly  
355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val  
370 375 380

Gly Thr Phe Val Thr Pro Ieu Ser Pro Ala Leu Trp Met Gly I [REDACTED] Gly  
 385 390 [REDACTED] 395 [REDACTED] 400  
 Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp  
 405 410 [REDACTED] 415  
 Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly  
 420 425 [REDACTED] 430  
 Ile Val Pro Leu Pro  
 435

<210> 60  
 <211> 1155  
 <212> DNA  
 <213> Neisseria gonorrhoeae

<220>  
 <221> CDS  
 <222> (1)...(1152)

<400> 60 48  
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 Met Gly Ile His Leu Asp Phe Gly Ile Ser Pro Lys Thr Phe Arg Gln  
 1 5 10 15  
 act tat ctg tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat 96  
 Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn  
 20 25 30  
 ctc gaa gcc gca tct tgt aaa tat atc aac gag ata tac caa cga gca 144  
 Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala  
 35 40 45  
 gac cca acc gca ccg ctg ttt cat ctg cgt aaa aaa ggc gca atc gtt 192  
 Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Gly Ala Ile Val  
 50 55 60  
 cct aaa gaa gaa tac gtc gaa agt ttc gac gat ttg ggc aaa act cgc 240  
 Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg  
 65 70 75 80  
 tac cgt ttt att aaa tcc gtt atc tac gaa cat atg aag aat ggt gcg 288  
 Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala  
 85 90 95  
 tcg tta gtc tat aac cat att aac aac gag ccg ttt tca gac cat atc 336  
 Ser Leu Val Tyr Asn His Ile Asn Glu Pro Phe Ser Asp His Ile  
 100 105 110  
 gcc cgt caa gtc gcc cgc ttt gcc ggc gca cat act att gtt agt gga 384  
 Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly  
 115 120 125  
 tat ctt gct ttt ggc agc gac gaa tct tat aaa aac cat tgg gat acc 432  
 Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr  
 130 135 140  
 cgc gat gtg tat gcc atc cag ctt ttc ggc aag aaa cgt tgg caa ctt 480  
 Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu  
 145 150 155 160  
 act gcc cct gat ttc cct atg cca ttg tat atg caa cag act aaa gat 528

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp  
 165 170 175  
 act gat att tcc att cct gaa cat atc gat atg gat att atc ctt gaa 576  
 Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu  
 180 185 190  
 gca ggt gat gtc ctc tac atc cca cgc ggt tgg tgg cac aga cct atc 624  
 Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile  
 195 200 205  
 ccg ctc ggc tgt gaa acc ttc cac ttc gct gtc ggt acc ttc cca cca 672  
 Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro  
 210 215 220  
 aac ggc tat aat tac ctc gag tgg cta atg aag aaa ttt ccc acc ata 720  
 Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile  
 225 230 235 240  
 gaa agt ctg cgc cac agt ttc tca gac tgg gag caa gat agg acg cgt 768  
 Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg  
 245 250 255  
 atc aac gat act gcc gca caa att gct gcc atg att gcc gac ccc gtc 816  
 Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val  
 260 265 270  
 aat tat gaa gcc ttc agt gaa gac ttt ctc ggc aaa gaa cgt acc gat 864  
 Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp  
 275 280 285  
 acc gct ttt cat ctc gaa cag ttc gcg aat ccc aac gct act ccg ctt 912  
 Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu  
 290 295 300  
 tca gac gac gtc agg ttg aga tta aat gcc aat aat ttg gat acg ttg 960  
 Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu  
 305 310 315 320  
 gaa aag gga tat ttg att ggg aat ggg atg aag ata agc gta gat gag 1008  
 Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu  
 325 330 335  
 ttg ggg aaa aaa gtg tta gaa cac atc ggt aag aat gaa ccg tta ttg 1056  
 Leu Gly Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu  
 340 345 350  
 ttg aaa aat cta ctg gtt aac ttc aat cag gca aaa cat gaa gaa gtt 1104  
 Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val  
 355 360 365  
 agg aag ttg atc tat cag ttg ata gag tta gat ttt ctg gaa att ttg 1152  
 Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Ile Leu  
 370 375 380  
 tga 1155

<210> 61  
 <211> 384  
 <212> PRT  
 <213> Neisseria gonorrhoeae

<400> 61  
 Met Gly Ile His Leu Asp Phe Gly Ile Ser Pro Lys Thr Phe Arg Gln  
 1 5 10 15

Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val A Asn  
20 25 30

Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala  
35 40 45

Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val  
50 55 60

Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg  
65 70 75 80

Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala  
85 90 95

Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile  
100 105 110

Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly  
115 120 125

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr  
130 135 140

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu  
145 150 155 160

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp  
165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu  
180 185 190

Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile  
195 200 205

Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro  
210 215 220

Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile  
225 230 235 240

Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg  
245 250 255

Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val  
260 265 270

Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp  
275 280 285

Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu  
290 295 300

Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu  
305 310 315 320

Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu  
325 330 335

Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu  
340 345 350

Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val  
355 360 365

Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu I<sup>Y</sup> Leu  
370 375 380

<210> 62  
<211> 717  
<212> DNA  
<213> Neisseria meningitidis

<220>  
<221> CDS  
<222> (1)..(714)

<400> 62  
atg aat aga ccc aag caa ccc ttc ttc cgt ccc gaa gtc gcc gtt gcc 48  
Met Asn Arg Pro Lys Gln Pro Phe Phe Arg Pro Glu Val Ala Val Ala  
1 5 10 15  
  
cgc caa acc agc ctg acg ggt aaa gtg att ctg aca cga ccg ttg tca 96  
Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser  
20 25 30  
  
ttt tcc cta tgg acg aca ttt gca tcg ata tct gcg tta ttg att atc 144  
Phe Ser Leu Trp Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile  
35 40 45  
  
ctg ttt ttg ata ttt ggt aac tat acg cga aag aca aca gtg gag gga 192  
Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Val Glu Gly  
50 55 60  
  
caa att tta cct gca tcg ggc gta atc agg gtg tat gca ccg gat acg 240  
Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr  
65 70 75 80  
  
ggg aca att aca gcg aaa ttc gtg gaa gat gga gaa aag gtt aag gct 288  
Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala  
85 90 95  
  
ggc gac aag cta ttt gcg ctt tcg acc tca cgt ttc ggc gca gga gat 336  
Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp  
100 105 110  
  
agc gtg cag cag cag ttg aaa acg gag gca gtt ttg aag aaa acg ttg 384  
Ser Val Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu  
115 120 125  
  
gca gaa cag gaa ctg ggt cgt ctg aag ctg ata cac ggg aat gaa acg 432  
Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr  
130 135 140  
  
cgc agc ctt aaa gca act gtc gaa cgt ttg gaa aac cag gaa ctc cat 480  
Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Glu Leu His  
145 150 155 160  
  
att tcg caa cag ata gac ggt cag aaa agg cgc att aga ctt gcg gaa 528  
Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu  
165 170 175  
  
gaa atg ttg cag aaa tat cgt ttc cta tcc gcc aat gat gca gtg cca 576  
Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro  
180 185 190  
  
aaa caa gaa atg atg aat gtc aag gca gag ctt tta gag cag aaa gcc 624  
Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Glu Gln Lys Ala

195

200

205

aaa ctt gat gcc tac' cgc a gaa gaa gtc ggg ctg ctt cag s atc 672  
 Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile  
 210 215 220

cgc acg cag aat ctg aca ttg gcc agc ctc ccc caa gcg gca tga 717  
 Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala  
 225 230 235

&lt;210&gt; 63

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Neisseria meningitidis

&lt;400&gt; 63

Met Asn Arg Pro Lys Gln Pro Phe Phe Arg Pro Glu Val Ala Val Ala  
 1 5 10 15

Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser  
 20 25 30

Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile  
 35 40 45

Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly  
 50 55 60

Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr  
 65 70 75 80

Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala  
 85 90 95

Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp  
 100 105 110

Ser Val Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu  
 115 120 125

Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr  
 130 135 140

Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Glu Leu His  
 145 150 155 160

Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu  
 165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro  
 180 185 190

Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala  
 195 200 205

Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile  
 210 215 220

Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala  
 225 230 235

&lt;210&gt; 64

&lt;211&gt; 690

<212> DNA  
<213> Neisseria gonorrhoeae  
  
<220>  
<221> CDS  
<222> (1)..(687)

<400> 64  
atg atg aat gtc gag gca gag ctt tta gag cag aaa gcc aaa ctt gat 48  
Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp  
1 5 10 15  
  
gcc tac ggc cga gaa gaa gcc ggg ctg ctt cag gaa atc cgc acg cag 96  
Ala Tyr Gly Arg Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln  
20 25 30  
  
aat ctg aca ttg gcc agc ctc ccc aaa cgg cat gag aca gaa caa agc 144  
Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser  
35 40 45  
  
cag ctt gaa cgc acc atg gcc gat att tct caa gaa gtt ttg gat ttt 192  
Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe  
50 55 60  
  
gaa atg cgc tct gaa caa atc atc cgt gca gga cgg tcg ggt tat ata 240  
Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile  
65 70 75 80  
  
gca ata ccg aac gtc gaa gtc gga cgg cag gtt gat cct tcc aaa ctg 288  
Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu  
85 90 95  
  
ctc ttg agc att gtt ccc gaa cgt acc gag tta tat gcc cat cta tat 336  
Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr  
100 105 110  
  
atc ccc agc agt gca gca ggc ttt atc aag ccg aaa gac aag gtt gtc 384  
Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val  
115 120 125  
  
cta cgt tat cag gca tat ccc tat cag aaa ttc ggg ctt gct tcc ggc 432  
Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly  
130 135 140  
  
agt gtc gta tca gtg gca aaa acg gca ctg ggc aga cag gaa ttg tcg 480  
Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser  
145 150 155 160  
  
gga ttg ggc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt 528  
Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val  
165 170 175  
  
tat ctc gtg aaa ata aaa ccc gac aaa cca acc atc act gca tac ggt 576  
Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly  
180 185 190  
  
gag gaa aaa ccg ctg caa atc ggc atg acg ctg gaa gca gac atc cta 624  
Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu  
195 200 205  
  
cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag ccg att tac agt 672  
His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser  
210 215 220  
  
atg tcg ggc agg ttg taa 690  
Met Ser Gly Arg Leu

<210> 65  
<211> 229  
<212> PRT  
<213> Neisseria gonorrhoeae

<400> 65  
Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp  
1 5 10 15  
Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln  
20 25 30  
Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser  
35 40 45  
Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe  
50 55 60  
Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile  
65 70 75 80  
Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu  
85 90 95  
Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr  
100 105 110  
Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val  
115 120 125  
Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly  
130 135 140  
Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser  
145 150 155 160  
Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val  
165 170 175  
Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly  
180 185 190  
Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu  
195 200 205  
His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser  
210 215 220  
Met Ser Gly Arg Leu  
225

<210> 66  
<211> 924  
<212> DNA  
<213> Neisseria gonorrhoeae

<220>  
<221> CDS  
<222> (1)..(921)

<400> 66

atg caa tac agc aca ctg gca gga caa acc gac aac tcc ctc gtt tcc Met Gln Tyr Ser Thr Leu [REDACTED] Gly Gln Thr Asp Asn Ser Leu [REDACTED] Ser	1                   5                   10	48
aat aat ttc ggg ttt ttg cgc ctg ccg ctt aat ttt atg ccg tat gaa Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu	20                   25                   30	96
agc cat gcc gat tgg gtt att acc ggc gtg cct tat gat atg gcg gtt Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val	35                   40                   45	144
tca ggg cgt tcc ggc gcg cgt ttc ggt cct gaa gcc atc cgg cgc gcc Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala	50                   55                   60	192
tcc gtc aac ctc gct tgg gag cac cgc agg ttt ccg tgg aca ttt gat Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp	65                   70                   75                   80	240
gtg cgc gaa cgc ctg aac att att gat tgc ggc gac ttg gtt ttt tct Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser	85                   90                   95	288
ttt ggc gac agc agg gat ttt gtc gaa aaa atg gaa gcg cac gcc ggc Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly	100                   105                   110	336
aaa tta ctt tct ttc ggc aaa cgc tgt ttg agt ttg ggc ggc gac cat Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His	115                   120                   125	384
ttc att acc ctc ccg ttg ttg cgc gcc cac gcc cgc tat ttc ggc aaa Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys	130                   135                   140	432
ctc gca ctg att cat ttt gac gcg cac acc gac acc tac gac aac ggc Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly	145                   150                   155                   160	480
agc gaa tac gac cac ggc acg atg ttt tat acc gcc ccc aag gaa ggc Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly	165                   170                   175	528
ctc atc gac ccg tcc cgt tcc gta caa atc ggc ata cgc acc gaa cac Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His	180                   185                   190	576
agt aaa aaa ttg cct ttt act gtg ttg tcc gcc ccc aaa gtc aat gaa Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu	195                   200                   205	624
gac agt gtt gaa gag acc gtc cgt aaa atc aaa gaa acc gtc ggc aat Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn	210                   215                   220	672
atg ccc gtt tac ctg act ttc gac ata gac tgt ctc gac ccg tcg ttc Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe	225                   230                   235                   240	720
gcc ccc ggg acc ggt acg ccc gta tgc ggc ggc ttg agc agc gac agg Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg	245                   250                   255	768
gca tta aaa atc cta cgt ggg ctg acg gat ctc gac atc gtc ggt atg Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met	2816	

260

265

270

gat gtt gta gaa gtt' gc c tct tac gac caa tcc gac att gct 864  
 Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala  
 275 280 285

ttg gcc ggc gcc aca att gcc ttg gaa atg ctt tac ctt caa ggt gcg 912  
 Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala  
 290 295 300

aaa aag gac tga 924  
 Lys Lys Asp  
 305

<210> 67  
 <211> 307  
 <212> PRT  
 <213> Neisseria gonorrhoeae

<400> 67  
 Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser 15  
 1 5 10 15

Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu 30  
 20 25 30

Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val 45  
 35 40 45

Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala 60  
 50 55 60

Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp 80  
 65 70 75 80

Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser 95  
 85 90 95

Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly 110  
 100 105 110

Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His 125  
 115 120 125

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys 140  
 130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly 160  
 145 150 155 160

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly 175  
 165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His 190  
 180 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu 205  
 195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn 220  
 210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe 240  
 225 230 235 240

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg  
245 250

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met  
260 265 270

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala  
275 280 285

Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala  
290 295 300

Lys Lys Asp  
305

<210> 68  
<211> 1404  
<212> DNA  
<213> Neisseria meningitidis

<220>  
<221> CDS  
<222> (1)..(1401)

<400> 68  
atg aca ttg ctc aat cta atg ata atg caa gat tac ggt att tcc gtt 48  
Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val  
1 5 10 15

tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tcg gct atg 96  
Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met  
20 25 30

aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144  
Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu  
35 40 45

cca cta tcc ctt tcc cca tcc gtt tcg gct ttt acg ctg cct gaa gca 192  
Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala  
50 55 60

tgg cgg gcg gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac 240  
Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr  
65 70 75 80

cag cgt gat gca gtg cgc gca cgg caa caa caa gcc aag gcc gca ttc 288  
Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Ala Lys Ala Ala Phe  
85 90 95

ctt ccc cat gta tcc gcc aat gcc agc tac cag cgc cag ccg cca tcg 336  
Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser  
100 105 110

att tct tcc acc cgc gaa aca cag gga tgg agc gtg cag gtg gga caa 384  
Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln  
115 120 125

acc tta ttt gac gct gcc aaa ttt gca caa tac cgc caa agc agg ttc 432  
Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe  
130 135 140

gat acg cag gct gca gaa cag cgt ttc gat gcg gca cgc gaa gaa ttg 480  
Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu  
145 150 155 160

ctg ttg aaa gtt gcc gaa	tat ttc aac gtt tta ctc agc	gac	528
Leu Leu Lys Val Ala Glu	Tyr Phe Asn Val Leu Leu Ser	Asp	
165	170	175	
acc gtt gcc gcc cat gcg	gcg gaa aaa gag gct tat gcc cag cag gta		576
Thr Val Ala Ala His Ala	Glu Lys Glu Ala Tyr Ala Gln Gln Val		
180	185	190	
agg cag gcg cag gct tta	tac aat aaa ggt gct gcc acc gcg ctg gat		624
Arg Gln Ala Gln Ala Leu	Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp		
195	200	205	
att cac gaa gcc aaa gcc	ggt tac gac aat gcc ctg gcc caa gaa atc		672
Ile His Glu Ala Lys Ala	Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile		
210	215	220	
gcc gta ttg gct gag aaa	caa acc tat gaa aac cag ttg aac gac tac		720
Ala Val Leu Ala Glu Lys	Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr		
225	230	235	240
acc gac ctg gat agc aaa	caa atc gag gcc ata gat acc gcc aac ctg		768
Thr Asp Leu Asp Ser Lys	Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu		
245	250	255	
ttg gca cgc tat ctg ccc	aag ctg gaa cgt tac agt ctg gat gaa tgg		816
Leu Ala Arg Tyr Leu Pro	Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp		
260	265	270	
cag cgc att gcc tta tcc	aac aat cat gaa tac cgg atg cag cag ctt		864
Gln Arg Ile Ala Leu Ser	Asn Asn His Glu Tyr Arg Met Gln Gln Leu		
275	280	285	
gcc ctg caa agc agc gga	cag gcg ctt cgg gca gca cag aac agc cgc		912
Ala Leu Gln Ser Ser Gly	Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg		
290	295	300	
tat ccc acc gtt tct gcc	cat gtc ggc tat cag aat aac ctc tac act		960
Tyr Pro Thr Val Ser Ala	His Val Gly Tyr Gln Asn Asn Leu Tyr Thr		
305	310	315	320
tca tct gcg cag aat aat	gac tac cac tat cgg ggc aaa ggg atg agc		1008
Ser Ser Ala Gln Asn Asp	Tyr His Tyr Arg Gly Lys Gly Met Ser		
325	330	335	
gtc ggc gta cag ttg aat	ttg ccg ctt tat acc ggc gga gaa ttg tcg		1056
Val Gly Val Gln Leu Asn	Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser		
340	345	350	
ggc aaa atc cat gaa gcc	gaa gcg caa tac ggg gcc gcc gaa gca cag		1104
Gly Lys Ile His Glu Ala	Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln		
355	360	365	
ctg acc gca acc gag cg	g c ac atc aaa ctc gcc gta cgc cag gct tat		1152
Leu Thr Ala Thr Glu Arg	His Ile Lys Leu Ala Val Arg Gln Ala Tyr		
370	375	380	
acc gaa agc ggt gcg	gcg cgt tac caa atc atg gcg caa gaa cgg gtt		1200
Thr Glu Ser Gly Ala Al	Arg Tyr Gln Ile Met Ala Gln Glu Arg Val		
385	390	395	400
ttg gaa agc agc cgt ttg	aaa ctg aaa tcg acc gaa acc ggc caa caa		1248
Leu Glu Ser Ser Arg Leu	Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln		
405	410	415	
tac ggc atc cgc aac cgg	ctg gaa gta ata cgg gcg cgg cag gaa gtc		1296

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val

420

425

430

gcc caa gca gaa cag aaa ctg gct caa gca cggtataaa ttc atg ctg  
Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu  
435 440 445

1344

gct tat ttg cgc ttg gtg aaa gag agc ggg tta ggg ttg gaa acg gta  
Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val  
450 455 460

1392

ttt gcg gaa taa  
Phe Ala Glu  
465

1404

<210> 69  
<211> 467  
<212> PRT  
<213> Neisseria meningitidis

<400> 69  
Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val  
1 5 10 15

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met  
20 25 30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu  
35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala  
50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr  
65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe  
85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser  
100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln  
115 120 125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe  
130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu  
145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp  
165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val  
180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp  
195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile  
210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr  
225 230 235 240

Thr Asp Leu Asp Ser Lys Ile Glu Ala Ile Asp Thr Ala Leu  
245 250

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp  
260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu  
275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg  
290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr  
305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser  
325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser  
340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln  
355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr  
370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val  
385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln  
405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val  
420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu  
435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val  
450 455 460

Phe Ala Glu  
465

<210> 70  
<211> 696  
<212> DNA  
<213> Neisseria gonorrhoeae

<220>  
<221> CDS  
<222> (1)..(693)

<400> 70  
atg aaa caa tcc gcc cga ata aaa aat atg gat cag aca tta aaa aat 48  
Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn  
1 5 10 15

aca ttg ggc att tgc gcg ctt tta gcc ttt tgt ttt ggc gcg gcc atc 96  
Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile  
20 25 30

gca tca ggt tat cac ttg gaa tat gaa tac ggc tac cgt tat tct gcc 144  
Ala Ser Gly Tyr His Leu Lu Tyr Glu Tyr Gly Tyr Arg Tyr Ala  
35 40 45

gtg ggc gct ttg gct tcg gtt gta ttt tta tta ttg gca cgc ggc 192  
Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Ala Arg Gly  
50 55 60

ttc ccg cgc gtt tct tca gtt tta ctg att tac gtc ggc aca acc 240  
Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr  
65 70 75 80

gcc cta tat ttg ccg gtc ggc tgg ctg tat ggt gcg cct tct tat cag 288  
Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln  
85 90 95

ata gtc ggt tcg ata ttg gaa agc aat cct gcc gag gcg cgt gaa ttt 336  
Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe  
100 105 110

gtc ggc aat ctt ccc ggg tcg ctt tat ttt gtg cag gca tta ttt ttc 384  
Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe  
115 120 125

att ttt ggc ttg aca gtt tgg aaa tat tgt gta tct gtg ggg gta ttt 432  
Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe  
130 135 140

gct gac gta aaa aac tat aaa cgt cgc agc aaa ata tgg ctg acc ata 480  
Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile  
145 150 155 160

tta ttg act ttg att ttg tcc tgc gcg gtg atg gag aaa atc gcc ggc 528  
Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly  
165 170 175

gat aaa gat tgg cga gaa cct gat gcc ggc ctg ttg ttg aat att ttc 576  
Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe  
180 185 190

gac ctg tat tac gac ttg gct ttc cgc gcc ggc aca ata tgc cgc caa 624  
Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln  
195 200 205

gcg cgc cca cat ttt gga agc agc aaa aaa agc gtc aac atg gca tat 672  
Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr  
210 215 220

ccg cca act tgc gcc caa gta taa 696  
Pro Pro Thr Cys Ala Gln Val  
225 230

<210> 71  
<211> 231  
<212> PRT  
<213> Neisseria gonorrhoeae

<400> 71  
Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn  
1 5 10 15

Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile  
20 25 30

Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala

35

40

45

Val Gly Ala Leu Ala' Ser 51 Val Phe Leu Leu Leu Ala . Gly  
 50 55 60

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr  
 65 70 75 80

Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln  
 85 90 95

Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe  
 100 105 110

Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe  
 115 120 125

Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe  
 130 135 140

Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile  
 145 150 155 160

Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly  
 165 170 175

Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe  
 180 185 190

Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln  
 195 200 205

Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr  
 210 215 220

Pro Pro Thr Cys Ala Gln Val  
 225 230

<210> 72  
<211> 2607  
<212> DNA  
<213> Neisseria meningitidis

<220>  
<221> CDS  
<222> (1)..(2604)

<400> 72  
atg gct gcc aac caa cgt tac cgc aaa ccg ctg ccc ggt acg gat ttg 48  
Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu  
1 5 10 15

gaa tac tac gac gcg cgt gcg tgt gag ggc atc aaa ccc ggc tct 96  
Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser  
20 25 30

tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144  
Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val  
35 40 45

aac cgc gcg gac aaa gtc gat ttg ccg acg ctg caa agc tgg ctg ggt 192  
Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly  
50 55 60

cag ctg att gag gga aaa cag gaa atc gac ttt cct tgg tat ccg gcg Gln Leu Ile Glu Gly Ly[7] Gln Glu Ile Asp Phe Pro Trp Tyr [80] 65	75	80	240
cg[7] gtg gtg tgc cac gat att ctg ggg cag acc gcg ttg gtg gat ttg Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu 85	90	95	288
gca ggt ctg cgc gat gcg att gcc gaa aaa ggc ggc gat cct gcc aaa Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys 100	105	110	336
gtg aat ccg gtg gtg caa acc cag ctc atc gtc gac cac tcg ctg gcg Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala 115	120	125	384
gtg gaa tgc ggc ggc tac gac ccc gat gcg ttc cgc aaa aac cgc gaa Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu 130	135	140	432
atc gaa gac aga cgt aac gaa gac cgt ttc cac ttc atc aac tgg aca Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr 145	150	155	480
aaa acc gct ttt gaa aat gtg gac gtg att ccg gcg ggc aac ggc atc Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile 165	170	175	528
atg cac caa atc aat cta gaa aaa atg tcg ccc gtc gtc caa gtc aaa Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys 180	185	190	576
aac ggc gtg gct ttc ccc gat acc tgc gtc ggc acg gat tcg cac acg Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr 195	200	205	624
cca cac gtc gat gcg ctg ggc gtg att tcc gtg ggc gtg ggc gga ttg Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu 210	215	220	672
gaa gcg gaa acc gta atg ctg gga cgc gcg tcc atg atg cgc ctg ccc Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro 225	230	235	720
gat att gtc ggc gtt gag ctg aac ggc aaa cgg aag gcg ggc att acg Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr 245	250	255	768
gcg acg gat att gtg ttg gca ctg acc gag ttt ctg cgc aaa gaa cgc Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg 260	265	270	816
gtg gtc ggg gcg ttt gtc gaa ttc ttg ggc gag ggc gcg aga agc ctg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu 275	280	285	864
tct atc ggc gac cgc gcg acc att tcc aac atg acg ccg gag ttg ggc Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly 290	295	300	912
gcg act gcc gcg atg ttg gct att gat gag caa acc att gat tat ttg Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu 305	310	315	960
aaa ctg acc gga cgc gac gac gcg cag gtg aaa ttg gtg gaa acc tac Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr			1008

325

330

335

gcc aaa acc gca ggc' tt~~g~~ gca gat gcc ttg aaa acc gcc ~~tat~~  
 Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr  
 340 345 350

1056

ccg cgc gtt ttg aaa ttt gat ttg agc agc gta acg cgc aat atg gca  
 Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala  
 355 360 365

1104

ggc ccg agc aac ccg cac gcg cgt ttt gcg acc gcc gat ttg gcc ggc  
 Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly  
 370 375 380

1152

aaa ggc ttg gct aaa cct tac gaa gag cct tca gac ggc caa atg cct  
 Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro  
 385 390 395 400

1200

gac ggt gca gtg att att gcc gcg att act tcc tgt acc aat act tcc  
 Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser  
 405 410 415

1248

aat ccg cgc aac gtt gtc gcc gcc ctg ttg gca cgc aat gcc aac  
 Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala Asn  
 420 425 430

1296

ccg ctc ggc ttg caa cgc aaa cct tgg gtg aaa tct tcg ttt gcc ccc  
 Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro  
 435 440 445

1344

gg~~t~~ tca aaa gta gcc gaa atc tat ttg aaa gaa gca gat ctg ctg ccc  
 Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro  
 450 455 460

1392

gaa atg gaa aaa ctc ggc ttc ggt atc gtt gcc ttc gca tgt acc acc  
 Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr  
 465 470 475 480

1440

tgt qac ggc atg agc ggc gcg ctg gat ccg aaa atc cag aaa gaa atc  
 Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile  
 485 490 495

1488

atc gac cgc gat ttg tac gcc acc gcc gta ttg tca ggc aac cgc aac  
 Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg Asn  
 500 505 510

1536

ttt gac ggc cgt atc cat ccg tat gcg aaa cag gct ttc ctc gct tcg  
 Phe Asp Gly Arg Ile His Pro Tyr Ala Lys Gln Ala Phe Leu Ala Ser  
 515 520 525

1584

cct ccg ttg gtc gtt gcc tac gcg ctg gca ggc agc atc cgt ttc gat  
 Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe Asp  
 530 535 540

1632

att gaa aac gac gta ctc ggc gtt gca gac ggc aaa gaa atc cgc ctg  
 Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu  
 545 550 555 560

1680

aaa gac att tgg cct acc gat gaa gaa atc gat gcc atc gtt gcc gaa  
 Lys Asp Ile Trp Pro Thr Asp Glu Glu Ile Asp Ala Ile Val Ala Glu  
 565 570 575

1728

tat gtg aaa ccg cag caa ttt cgc gac gtt tat atc ccg atg ttc gac  
 Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp  
 580 585 590

1776

acc ggc aca gcg caa aaa gca cca agc ccg ctg tac gac tgg cgt cca Thr Gly Thr Ala Gln Lysala Pro Ser Pro Leu Tyr Asp Trp A Pro 595	600	605	1824
atg tct acc tat atc cgc cgc cca cct tac tgg gaa ggc gca ctg gca Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala 610	615	620	1872
ggg gaa cgc aca tta agc ggt atg cgt ccg ctg gcg att ttg ccc gac Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp 625	630	635	1920
aac atc acc acc gac cat ctc tcg cca tcc aat gcg att ttg gca agc Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala Ser 645	650	655	1968
agt gcc gca ggc gaa tat ttg gca aaa atg ggt ttg cct gaa gaa gac Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Asp 660	665	670	2016
ttc aac tct tac gca acc cac cgt ggc gac cac ttg acc gcc caa cgc Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg 675	680	685	2064
gca acc ttc gcc aat ccg aaa ctg ttt aac gaa atg gtg aga aac gaa Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Arg Asn Glu 690	695	700	2112
gac ggc agc gta cgc caa ggt tcg ctg gca cgc gtt gaa ccc gaa ggc Asp Gly Ser Val Arg Gln Gly Ser Leu Ala Arg Val Glu Pro Glu Gly 705	710	715	2160
caa acc atg cgc atg tgg gaa gcc atc gaa acc tat atg aac cgc aaa Gln Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys 725	730	735	2208
cag ccg ctc atc atc att gcc ggc gcg gac tac ggt caa ggc tca agc Gln Pro Leu Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser Ser 740	745	750	2256
cgc gac tgg gct gca aaa ggc gta cgc ctc gcc ggc gtg gaa gcg att Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala Ile 755	760	765	2304
gtt gcc gaa ggc ttc gag cgt atc cac cgc acc aac ttg atc ggt atg Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met 770	775	780	2352
ggc gtg ttg ccg ctg cag ttc aaa ccg ggt acc aac cgc cac acc ctg Gly Val Leu Pro Leu Gln Phe Lys Pro Gly Thr Asn Arg His Thr Leu 785	790	795	2400
caa ctg gac ggt acg gaa acc tac gac gtt gtc ggc gaa cgc aca ccg Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro 805	810	815	2448
cgc tgc gac ctg acc ctt gtg att cac cgt aaa aac ggc gag acc gtc Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val 820	825	830	2496
gaa gtc ccc att acc tgc cgc ctc gat acc gca gaa gaa gtg ttg gta Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val 835	840	845	2544
tat gaa gcc ggt ggc gta ttg caa cgg ttt gca cag gat ttt ttg gaa Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu 850			2592

850

855

860

2607

ggg aac gcg gct tag'

Gly Asn Ala Ala

865

&lt;210&gt; 73

&lt;211&gt; 868

&lt;212&gt; PRT

&lt;213&gt; Neisseria meningitidis

&lt;400&gt; 73

Met	Ala	Ala	Asn	Gln	Arg	Tyr	Arg	Lys	Pro	Leu	Pro	Gly	Thr	Asp	Leu
1				5				10					15		

Glu	Tyr	Tyr	Asp	Ala	Arg	Ala	Ala	Cys	Glu	Gly	Ile	Lys	Pro	Gly	Ser
				20				25				30			

Tyr	Asp	Lys	Leu	Pro	Tyr	Thr	Ser	Arg	Ile	Leu	Ala	Glu	Asn	Leu	Val
					35			40				45			

Asn	Arg	Ala	Asp	Lys	Val	Asp	Leu	Pro	Thr	Leu	Gln	Ser	Trp	Leu	Gly
				50			55				60				

Gln	Leu	Ile	Glu	Gly	Lys	Gln	Glu	Ile	Asp	Phe	Pro	Trp	Tyr	Pro	Ala
				65			70			75			80		

Arg	Val	Val	Cys	His	Asp	Ile	Leu	Gly	Gln	Thr	Ala	Leu	Val	Asp	Leu
					85			90					95		

Ala	Gly	Leu	Arg	Asp	Ala	Ile	Ala	Glu	Lys	Gly	Gly	Asp	Pro	Ala	Lys
					100			105				110			

Val	Asn	Pro	Val	Val	Gln	Thr	Gln	Leu	Ile	Val	Asp	His	Ser	Leu	Ala
						115		120			125				

Val	Glu	Cys	Gly	Gly	Tyr	Asp	Pro	Asp	Ala	Phe	Arg	Lys	Asn	Arg	Glu
					130			135			140				

Ile	Glu	Asp	Arg	Arg	Asn	Glu	Asp	Arg	Phe	His	Phe	Ile	Asn	Trp	Thr
					145			150			155			160	

Lys	Thr	Ala	Phe	Glu	Asn	Val	Asp	Val	Ile	Pro	Ala	Gly	Asn	Gly	Ile
					165			170			175				

Met	His	Gln	Ile	Asn	Leu	Glu	Lys	Met	Ser	Pro	Val	Val	Gln	Val	Lys
					180			185			190				

Asn	Gly	Val	Ala	Phe	Pro	Asp	Thr	Cys	Val	Gly	Thr	Asp	Ser	His	Thr
					195			200			205				

Pro	His	Val	Asp	Ala	Leu	Gly	Val	Ile	Ser	Val	Gly	Val	Gly	Gly	Leu
					210			215			220				

Glu	Ala	Glu	Thr	Val	Met	Leu	Gly	Arg	Ala	Ser	Met	Met	Arg	Leu	Pro
					225			230			235			240	

Asp	Ile	Val	Gly	Val	Glu	Leu	Asn	Gly	Lys	Arg	Lys	Ala	Gly	Ile	Thr
					245			250			255				

Ala	Thr	Asp	Ile	Val	Leu	Ala	Leu	Thr	Glu	Phe	Leu	Arg	Lys	Glu	Arg
					260			265			270				

Val	Val	Gly	Ala	Phe	Val	Glu	Phe	Phe	Gly	Glu	Gly	Ala	Arg	Ser	Leu
					275			280			285				

Ser Ile Gly Asp Arg Ala **Ile** Ser Asn Met Thr Pro Glu **Ile** Gly  
290 5 300

Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu  
305 310 315 320

Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr  
325 330 335

Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr  
340 345 350

Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala  
355 360 365

Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly  
370 375 380

Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro  
385 390 395 400

Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser  
405 410 415

Asn Pro Arg Asn Val Val Ala Ala Leu Leu Ala Arg Asn Ala Asn  
420 425 430

Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro  
435 440 445

Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro  
450 455 460

Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr  
465 470 475 480

Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile  
485 490 495

Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg Asn  
500 505 510

Phe Asp Gly Arg Ile His Pro Tyr Ala Lys Gln Ala Phe Leu Ala Ser  
515 520 525

Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe Asp  
530 535 540

Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu  
545 550 555 560

Lys Asp Ile Trp Pro Thr Asp Glu Glu Ile Asp Ala Ile Val Ala Glu  
565 570 575

Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp  
580 585 590

Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg Pro  
595 600 605

Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala  
610 615 620

Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp  
625 630 635 640

Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ser  
645 650

Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Asp  
660 665 670

Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg  
675 680 685

Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Arg Asn Glu  
690 695 700

Asp Gly Ser Val Arg Gln Gly Ser Leu Ala Arg Val Glu Pro Glu Gly  
705 710 715 720

Gln Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys  
725 730 735

Gln Pro Leu Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser Ser  
740 745 750

Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala Ile  
755 760 765

Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met  
770 775 780

Gly Val Leu Pro Leu Gln Phe Lys Pro Gly Thr Asn Arg His Thr Leu  
785 790 795 800

Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro  
805 810 815

Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val  
820 825 830

Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val  
835 840 845

Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu  
850 855 860

Gly Asn Ala Ala  
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Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser  
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aaa ggc gtg ttt ttc aaa cgt tcc gac ctg ccc gag ggc gcg cgg gaa 96  
Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu  
20 25 30

gcg gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc ccg Ala Gly Ser Ala Arg Asp Ile Leu Leu Arg Val Leu Gly Pro	35                    40                    45	144
gat ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agc tcg tcc Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser	50                    55                    60	192
acc agc aag gcg gtg att ttg gac aag tcc gaa cgc gcc gat cac gat Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp	65                    70                    75                    80	240
gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp	85                    90                    95	288
tgg agt ggc aac tgc ggc aac ctc acc gcc gtc ggc gca ttt gcc Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala	100                    105                    110	336
atc gag caa ggc ttg gtc gat aaa ggc aag att cct tca gac ggc atc Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile	115                    120                    125	384
tgc aca gtc aaa atc tgg cag aaa aac atc ggc aaa acc att att gcc Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala	130                    135                    140	432
cat gta ccg atg caa aac ggc gca gtt ttg gaa aca ggc gat ttt gag His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu	145                    150                    155                    160	480
ctc gac ggc gta acg ttc ccg gca gcc gaa gta caa atc gaa ttt ctt Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu	165                    170                    175	528
gat cca gcc gac ggc gaa ggc agt atg ttc cca acc ggc aat ttg gtc Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val	180                    185                    190	576
gat gaa att gat gtg ccg aat ata ggc cgt ttg aaa gcc acg ctc atc Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile	195                    200                    205	624
aac gcg ggc att ccg acc gtt ttc ctg aat gcc gcc gac ttg ggc tac Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr	210                    215                    220	672
acg ggc aaa gag ttg caa gac gac atc aac aac gat gcc gca gct ttg Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Leu	225                    230                    235                    240	720
gaa aaa ttc gag aaa atc cgc gct tac ggt gcg ctg aaa atg ggt ctg Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu	245                    250                    255	768
atc agc gac gta tcc gaa gct gcc gcc cgc gcg cac acg ccg aaa gtc Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val	260                    265                    270	816
gcc ttc gtc gcg ccc gcc gat tac acc gcc tcc agt ggc aaa acc Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr	275                    280                    285	864
gtg aat gcc gcc gac atc gat ttg ctg gta cgc gcc ctg agc atg ggc Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly	290                    295                    300	912

290

295

300

aaa ttg cac cac gcg 'atg ggt acc gcc tct gtt gcc att [REDACTED] acc 960  
Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr  
305 310 315 . 320

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gcc gcc gcc gtg ccc ggt acg ctg gtc aac ctt gcc gca ggc ggc gga 1008
Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly
325          330          335

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acg cgt aaa gaa gtg cgc ttc ggg cat cct tcc ggc aca ttg cgc gtc 1056
Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
            340          345          350

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ggt gca gcc gcc gaa tgt cag gac gga caa tgg acg gcc acc aaa gcg      1104
Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
            355          360          365

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gtt atg agc cgc agc gca cgc gtg atg atg gaa ggt tgg gtc agg gtg 1152  
Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val  
370 375 380

ccg gaa gat tgt ttt taa . . . . . 1170  
Pro Glu Asp Cys Phe  
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<210> 75  
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<212> PRT  
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 Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu  
   20              25                 30  
  
 Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro  
   35              40                 45

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser  
       50                   55                   60

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp  
 65                   70                   75                   80  
 Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala  
 100 105 110

Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile  
115 120 125

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala  
130 135 140

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu  
145 150 155 160

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu  
165 170 175

Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val

180

185

190

Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile

195

200

205

Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr  
210 215 220

Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu  
225 230 235 240

Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu  
245 250 255

Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val  
260 265 270

Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr  
275 280 285

Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly  
290 295 300

Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr  
305 310 315 320

Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly  
325 330 335

Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val  
340 345 350

Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala  
355 360 365

Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val  
370 375 380

Pro Glu Asp Cys Phe  
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<210> 76

<211> 2094

<212> DNA

<213> Neisseria gonorrhoeae

<220>

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<222> (1)..(2091)

<400> 76

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ttc gcc tct ggc ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96  
Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg  
20 25 30

ctt cta ttc agc cac ata ggt atc gat ttg agt tcg att act gtc att 144  
Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile  
35 40 45

att tct gta ttt atg gtc ggc ttg ggt gta ggt gcg tat ttc ggc gga Ile Ser Val Phe Met Val Leu Gly Val Gly Ala Tyr Phe Gly	50                    55                    60	192
cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile	65                    70                    75                    80	240
gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc aag ggt ctg att Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile	85                    90                    95	288
tcc ggc ttg ggg cat ctt tta gtt gag gct gat ttg ccc atc atc gct Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala	100                    105                    110	336
gct gcc aat ttc ctc tta ttg ctg ctt cct acc ttt atg atg ggc gcg Ala Ala Asn Phe Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala	115                    120                    125	384
acc ttg ccc ttg ctg acc tgt ttt aac cg <sup>g</sup> aaa ata cat aat gtt Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val	130                    135                    140	432
ggc gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt gcg gca Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala	145                    150                    155                    160	480
ctc gga tcg ctt gcc gcc gaa ttt ttc tac gtc ttt ttt acc ctc Leu Gly Ser Leu Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu	165                    170                    175	528
tcc caa acc att gcg ctg aca gcc tgc ctt aac ctt ctg att gct gct Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Ile Ala Ala	180                    185                    190	576
tca gta tgc tgc gtt aca gaa agg atg gat atg gtg aac act aaa ccg Ser Val Cys Cys Val Thr Glu Arg Met Asp Met Val Asn Thr Lys Pro	195                    200                    205	624
aat act agt gtg att aat atg ctt tct ttc ctt acc gga tta ttg agc Asn Thr Ser Val Ile Asn Met Leu Ser Phe Leu Thr Gly Leu Leu Ser	210                    215                    220	672
ttg ggt ata gaa gtc ttg tgg gta agg atg ttt tcg ttc gca gca cag Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln	225                    230                    235                    240	720
tcc gtg cct cag gca ttt tca ttt att ctt gcc tgt ttt ctg acc ggt Ser Val Pro Gln Ala Phe Ser Phe Ile Leu Ala Cys Phe Leu Thr Gly	245                    250                    255	768
atc gcc gtc ggc gcg tat ttt ggc aaa cg <sup>g</sup> att tgc cgc agc cgc ttt Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe	260                    265                    270	816
gtt gat att ccc ttt atc ggg cag tgc ttc ttg tgg gcg ggt att gcc Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala	275                    280                    285	864
gat ttt ttg att ttg ggt gct gcg tgg ttg acg ggt ttt tcc ggt Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly	290                    295                    300	912
ttc gtc cac cac gcc ggt att ttc att acc ctg tct gcc gtc gtc agg Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg		960

305

310

315

320

ggg ttg att ttc cca'ctt a cac cat gtg ggt acg gat ggc  
 Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys  
 325 330 335

1008

tcc gga cga cag gtt tcc aat gtt tat ttc gcc aac gtt gcc ggc agt  
 Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser  
 340 345 350

1056

gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttg ttg tcc  
 Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser  
 355 360 365

1104

acc caa cag att tac ctg ctc atc tgt ttg att tct gct gct gtc cct  
 Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro  
 370 375 380

1152

ttg ttt tgt aca ctg ttc caa aaa agt ctc cga ctg aat gca gtg tcg  
 Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser  
 385 390 395 400

1200

gta gca gtt tcc cta atg ttc ggc atc ctc atg ttc cta ctg ccg gat  
 Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp  
 405 410 415

1248

tct gtc ttt caa aat att gct ggc cgt ccg gat agg ttg att gaa aac  
 Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn  
 420 425 430

1296

aaa cac ggc att gtt gcg gtt tac cat aga gat ggt gat aag gtt gtt  
 Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val  
 435 440 445

1344

tat ggg gcg aat gta tac gac ggc gca tac aat acc gat ata ttc aat  
 Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn  
 450 455 460

1392

agt gtc aac ggc atc gaa cgt gcc tat ctg cta ccc tcc ctg aag tcc  
 Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser  
 465 470 475 480

1440

ggc ata cgc cgc att ttc gtc gtt gga ttg agt aca ggt tcg tgg gcg  
 Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala  
 485 490 495

1488

cgc gtc ttg tct gcc att ccg gaa atg cag tcg atg atc gtt gcg gaa  
 Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu  
 500 505 510

1536

atc aat ccg gca tac cgt agc ctt atc gcg gac gag ccg caa atc gca  
 Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala  
 515 520 525

1584

ccg ctt ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt agg  
 Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg  
 530 535 540

1632

aaa tgg ctg cgt cgc cat cct gat gaa aaa ttc gac ctg att ttg atg  
 Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met  
 545 550 555 560

1680

aat tcg act tgg tac tgg cgt gcc tat tcc act aac ctg ttg agt gcg  
 Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala  
 565 570 575

1728

gaa ttt tta aaa cag gtg caa agc cac ctt acc ccg gat ggt att gta . 1776  
Glu Phe Leu Lys Gln Val Glu Ser His Leu Thr Pro Asp Gly Val  
580 . 585 . 590 .  
580 585 590

atg ttt aat acc acg cac agc ccg cat gct ttt gct acc gcc gta cac 1824  
Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His  
595 600 605  
595 600 605

agt att ccc tat gca tac cgc tac ggg cat atg gta gtc ggc tcg gca 1872  
Ser Ile Pro Tyr Ala Tyr Arg His Met Val Val Gly Ser Ala  
610 615 620  
610 615 620

acc ccg gta gtt ttc cct aat aaa gaa ctg ctc aag caa cgc ctt tcc 1920  
Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser  
625 630 635 640  
625 630 635 640

cggttg att tgg ccg gaa agc ggc agg cac gta ttt gac agc agc acc 1968  
Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr  
645 650 655  
645 650 655

gtg gat gct gca gca caa aag gtt gtc tct cgt atg ctg att cggtatg 2016  
Val Asp Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Arg Met  
660 665 670  
660 665 670

acg gaa cct tcg gct ggg gcg gaa gtc att act gac gat aat atg att 2064  
Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile  
675 680 685  
675 680 685

gta gaa tac aaa tac ggc aga ggg att taa 2094  
Val Glu Tyr Lys Tyr Gly Arg Gly Ile  
690 695  
690 695

<210> 77  
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<212> PRT  
<213> Neisseria gonorrhoeae

<400> 77  
Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe  
1 5 10 15  
1 5 10 15

Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg  
20 25 30  
20 25 30

Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile  
35 40 45  
35 40 45

Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly  
50 55 60  
50 55 60

Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile  
65 70 75 80  
65 70 75 80

Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile  
85 90 95  
85 90 95

Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala  
100 105 110  
100 105 110

Ala Ala Asn Phe Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala  
115 120 125  
115 120 125

Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val  
130 135 140  
130 135 140

Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala  
145 150 155 160

Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu  
165 170 175

Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Leu Ile Ala Ala  
180 185 190

Ser Val Cys Cys Val Thr Glu Arg Met Asp Met Val Asn Thr Lys Pro  
195 200 205

Asn Thr Ser Val Ile Asn Met Leu Ser Phe Leu Thr Gly Leu Leu Ser  
210 215 220

Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln  
225 230 235 240

Ser Val Pro Gln Ala Phe Ser Phe Ile Leu Ala Cys Phe Leu Thr Gly  
245 250 255

Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe  
260 265 270

Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala  
275 280 285

Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly  
290 295 300

Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg  
305 310 315 320

Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys  
325 330 335

Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser  
340 345 350

Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser  
355 360 365

Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro  
370 375 380

Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser  
385 390 395 400

Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp  
405 410 415

Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn  
420 425 430

Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val  
435 440 445

Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn  
450 455 460

Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser  
465 470 475 480

Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala  
485 490 495

Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu  
500 505 510

Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala  
515 520 525

Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg  
530 535 540

Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met  
545 550 555 560

Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala  
565 570 575

Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val  
580 585 590

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His  
595 600 605

Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala  
610 615 620

Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser  
625 630 635 640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr  
645 650 655

Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Arg Met  
660 665 670

Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile  
675 680 685

Val Glu Tyr Lys Tyr Gly Arg Gly Ile  
690 695

<210> 78

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<220>

<223> Description of Artificial Sequence: primer

<400> 78

gctctagacc accatgtctg aagaaaaatt gaaaatgag 39

<210> 79

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 79

cgggatccag aaatggctgg attcgctatc ag

32

<210> 80  
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<400> 80  
gctctagacc accatgaaac acttactcat cg

32

<210> 81  
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<223> Description of Artificial Sequence: primer

<400> 81  
cgggatccaa tacgttaggac ttgggtc

27

<210> 82  
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<212> DNA  
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<223> Description of Artificial Sequence: primer

<400> 82  
gctctagacc accatgaaaa aatcccttt cgttc

35

<210> 83  
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<400> 83  
cgggatccat tgcggataaa catattccgc c

31

<210> 84  
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<212> DNA  
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<223> Description of Artificial Sequence: primer

<400> 84  
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34

<210> 85  
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<223> Description of Artificial Sequence: primer

<400> 85

cgggatccag aaccggtagc ctacgccgac

30

<210> 86

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 86

gctctagacc accatgaaca cacgcacatcat cgtttc

36

<210> 87

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 87

cgggatccag caacggcctg ccgtttaag

30

<210> 88

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 88

gctctagacc accatgctga cgtttatcg actg

34

<210> 89

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 89

cgggatccac ggcagaggca cgattcc

27

<210> 90

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 90

gctctagacc accatgggca tccatctcga cttc

34

<210> 91  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 91  
cgggatccac aaaagttcca gaaaatctaa ctc

33

<210> 92  
<211> 33  
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<223> Description of Artificial Sequence: primer

<400> 92  
gctctagacc accatgaata gacccaagca acc

33

<210> 93  
<211> 26  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 93  
cgggatccat gccgcttggg ggaggc

26

<210> 94  
<211> 34  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 94  
gctctagacc accatgatga atgtcgaggc agag

34

<210> 95  
<211> 26  
<212> DNA  
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<223> Description of Artificial Sequence: primer

<400> 95  
cgggatccac agtttgcccc acatac

26

<210> 96  
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<212> DNA  
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<220>

<223> Description of Artificial Sequence: primer

<400> 96

gctctagacc accatgaaat ttttcctgc tcc

33

<210> 97

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 97

gaagatctag aaactgtaat tcaagttgaa ggaagatcta gaaactgtaa ttcaagttga 60

ag 62

<210> 98

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 98

gctctagacc accatgattt aatttgtccg agc

33

<210> 99

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 99

cgggatccaa ccctgcgacg agttgcgcgg gatccaaccc tgcgacgagt tgcg

54

<210> 100

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 100

gctctagacc accatgcaat acagcacact ggc

33

<210> 101

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 101

cgggatccag tccttttcg caccttgaag

30

<210> 102  
<211> 34  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 102  
gctctagacc accatggagc agtcgggcaa attc 34

<210> 103  
<211> 30  
<212> DNA  
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<220>  
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<400> 103  
cgggatccaa gctgttggc gatttcggtg 30

<210> 104  
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<220>  
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<400> 104  
gctctagacc accatgcaaa acggcgaaaa aaag 34

<210> 105  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 105  
cgggatccag tgcctgcgca gcttggaaatc 30

<210> 106  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 106  
gctctagacc accatgacat tgctcaatct aatgataatg 40

<210> 107  
<211> 33  
<212> DNA  
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<220>  
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<400> 107  
cgggatccat tccgcaaata cctgtttcca acc

33

<210> 108  
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<212> DNA  
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<400> 108  
gctctagacc accatgaaac aatccgccccg

30

<210> 109  
<211> 28  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 109  
cgggatccat acttgggcgc aacatgac

28

<210> 110  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 110  
gctctagacc accatgaatg ttacggttt ccc

33

<210> 111  
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<212> DNA  
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<220>  
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<400> 111  
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32

<210> 112  
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<220>  
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<400> 112  
gctctagacc accatgatga gtcaaacactc tgcc

34

40320\*\*E404860

<210> 113  
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<223> Description of Artificial Sequence: primer

<400> 113  
cgggatccat ccagttttg ctcaaggc 29

<210> 114  
<211> 34  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 114  
gctctagacc accatgcctt cgagcaaaaa ctgg 34

<210> 115  
<211> 32  
<212> DNA  
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<400> 115  
cgggatccat cgttcttcaa tctccacaaa cg 32

<210> 116  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 116  
gctctagacc accatgcacc tatgtggaaa g 31

<210> 117  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 117  
cgggatccat tcaattcgct tcaacaatg 29

<210> 118  
<211> 36  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 118  
ggactagtcc accatggctg c accaacg ttaccg

36

<210> 119  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 119  
gaagatctaa gccgcgttcc cttccaaaaa atc

33

<210> 120  
<211> 34  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 120  
gctctagacc accatgccgc aaattaaaaat tccc

34

<210> 121  
<211> 29  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 121  
cgggatccaa aaacaatctt ccggcaccc

29

<210> 122  
<211> 33  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 122  
gctctagacc accatgcgca cgccgttttg ttg

33

<210> 123  
<211> 29  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 123  
cgggatccat tgggcaacga cgaaggcac

29

<210> 124  
<211> 33

<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 124  
gctctagacc accatgagaa tagagatcac acc

33

<210> 125  
<211> 27  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer  
  
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cgggatccat ggctcaatcc tttctgc

27

<210> 126  
<211> 34  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 126  
gctctagacc accatgattc acgtttcggc agtg

34

<210> 127  
<211> 29  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 127  
cgggatccaa cctgcttcat gggtgattc

29

<210> 128  
<211> 36  
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<400> 128  
gctctagacc accatgaatt cgaccgcaag taaaac

36

<210> 129  
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<400> 129  
cgggatccaa atccctctgc cttatgg

28

709430 " E 4 file 360